



CC modulates the function of an apoptosis-associated polypeptide, particularly a kinase or GPCR (G-protein-coupled receptor). The method CC comprises providing a sample containing an apoptosis-activator, CC polypeptide and a candidate agent and incubating under conditions to CC permit binding of the candidate agent to the polypeptide, measuring the binding and comparing it with the binding of the polypeptide to a control agent known not to bind to the polypeptide. The method of the invention CC has cytostatic, antiinflammatory, antiallergic, respiratory, CC anti-rheumatic, antiulcer, gastrointestinal, immunosuppressive and neuroprotective applications. The method and molecules may be useful for CC treating a disease or condition characterised by abnormal apoptosis in mammalian tissue, particularly cancer, such as small cell lung cancer, CC cancer of the kidney, uterus, prostate, bladder, ovary, colon and breast, CC leukaemias, sarcomas and myelomas. Furthermore, autoimmune, CC neurodegenerative and inflammatory conditions may be treated, including CC arachnoiditis, chronic obstructive pulmonary disease, cystic fibrosis, CC rheumatoid arthritis, acute respiratory distress syndrome, preclampsia, CC myocardial ischaemia, reperfusion injury, psoriasis, bronchiolitis, CC Crohn's disease, ulcerative colitis and inflammatory bowel disease. The CC current sequence is that of a human apoptosis-associated protein of the CC invention which was used during siRNA (small interfering RNA)-mediated gene silencing.

CC Sequence 137 AA;

Query Match 100.0%; Score 725; DB 8; Length 137;

Best Local Similarity 100.0%; Pred. No. 6.3e-75; Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVTKPRYKQWRETMSTSSTLGFRIEGIKADGTCTNFRKTTQALEQVTKLEDFVGDHV 60  
Db 1 AVTKPRYKQWRETMSTSSTLGFRIEGIKADGTCTNFRKTTQALEQVTKLEDFVGDHV 60  
Qy 61 ILQKVVACELRERALEISPFKTHEVVGSSLLFVHDHGLAKWMIDFGKTVALPDHQI 120  
Db 61 ILQKVVACELRERALEISPFKTHEVVGSSLLFVHDHGLAKWMIDFGKTVALPDHQI 120  
Qy 121 LSHRLPWAGNREDGYL 137  
Db 121 LSHRLPWAGNREDGYL 137

RESULT 2

ID ABB09774 standard; protein; 604 AA.

AC ABB09774; DT 22-JUL-2002 (first entry)

DE Amino acid sequence of human inositol-1,4,5-triphosphate 3 kinase-C. KW IP3 kinase; inositol-1,4,5-triphosphate kinase; enzyme; oxidative stress; KW endoplasmic reticulum stress; neurodegeneration; retina; free radical; KW chronic infection; arthritis; cancer; cystic fibrosis; KW Alzheimer's disease; Huntington's disease; pigmentary retinopathy; KW DIP3K1; DIP3K2.

OS Homo sapiens.

XX FR2813612-A1.

XX PN

XX PR 07-SEP-2000; 2000FR-00011397.

XX PD 08-MAR-2002.

XX PI (CNRS ) CNRS CENT NAT RBCH SCI.

XX DR WPI: 2002-260343/31.  
XX N-PSDB: ABL56446.  
XX The present sequence represents inositol-1,4,5-triphosphate kinase activity, useful e.g. for PT treating oxidative stress and neurodegeneration.  
XX PS Claim 4; Fig 5; 69pp; French.  
XX The present sequence represents inositol-1,4,5-triphosphate kinase activity. The specification also describes Drosophila IP3 kinase kinase-C protein. The specification describes the use of IP3 kinase proteins to prepare compositions for treating disease associated with oxidative stress, stress of the endoplasmic reticulum or neurodegeneration, particularly of the retina. Overexpression of IP3 kinase protects cells against the damaging effects of free radicals without altering free radical homeostasis within the cell. The IP3 proteins are used for treating disorders associated with oxidative stress, stress on the endoplasmic reticulum and neurodegeneration, particularly chronic infection (such as arthritis and some forms of cancer); cystic fibrosis; Alzheimer's and Huntington's diseases, and pigmentary retinopathy. Transgenic animals that lack the gene for IP3 kinase proteins are used to identify phenotypic alterations associated with loss of this gene.  
XX Sequence 604 AA;  
XX Query Match 100.0%; Score 725; DB 5; Length 604;  
XX Best Local Similarity 100.0%; Pred. No. 4.9e-74; Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX Qy 1 AVTKPRYKQWRETMSTSSTLGFRIEGIKADGTCTNFRKTTQALEQVTKLEDFVGDHV 60  
Db 452 AVTKPRYKQWRETMSTSSTLGFRIEGIKADGTCTNFRKTTQALEQVTKLEDFVGDHV 511  
Qy 61 ILQKVVACELRERALEISPFKTHEVVGSSLLFVHDHGLAKWMIDFGKTVALPDHQI 120  
Db 512 ILQKVVACELRERALEISPFKTHEVVGSSLLFVHDHGLAKWMIDFGKTVALPDHQI 571  
Qy 121 LSHRLPWAGNREDGYL 137  
Db 572 LSHRLPWAGNREDGYL 588

RESULT 3

ID ABB09784 standard; protein; 604 AA.

AC ABB09784; DT 22-JUL-2002 (first entry)

DE Amino acid sequence of human inositol-1,4,5-triphosphate 3 kinase-C. KW IP3 kinase; inositol-1,4,5-triphosphate kinase; enzyme; oxidative stress; KW endoplasmic reticulum stress; neurodegeneration; retina; free radical; KW chronic infection; arthritis; cancer; cystic fibrosis; KW Alzheimer's disease; Huntington's disease; pigmentary retinopathy; KW DIP3K1; DIP3K2.

OS Homo sapiens.

XX FR200220742-A1.

XX PN

XX PR 31-AUG-2001; 2001MO-FR002708.

XX PD 07-SEP-2000; 2000FR-00011397.

XX PI Tricoire H, Monnier V, Pret AM, Cabet DE, Bressard J, Vandurka P; Girardot F;



**RESULT 5**  
 ID ABU65211  
 AC ABU65211;  
 XX DT 20-MAY-2003 (first entry)  
 XX DE Human NOV123a protein.  
 XX KW NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;  
 KW hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;  
 KW human.  
 XX OS Homo sapiens.  
 XX PN WO200272757-A2.  
 XX PD 19-SEP-2002.  
 XX PF 08-MAR-2002; 2002WO-US006908.  
 XX PR 08-MAR-2001; 2001US-0374101P.  
 PR 08-MAR-2001; 2001US-0274194P.  
 PR 08-MAR-2001; 2001US-024281P.  
 PR 09-MAR-2001; 2001US-0274322P.  
 PR 11-MAR-2001; 2001US-0274849P.  
 PR 12-MAR-2001; 2001US-0215235P.  
 PR 13-MAR-2001; 2001US-0275578P.  
 PR 13-MAR-2001; 2001US-0275601P.  
 PR 14-MAR-2001; 2001US-0276776P.  
 PR 16-MAR-2001; 2001US-0276994P.  
 PR 19-MAR-2001; 2001US-0277239P.  
 PR 20-MAR-2001; 2001US-0277321P.  
 PR 20-MAR-2001; 2001US-0277327P.  
 PR 21-MAR-2001; 2001US-0277791P.  
 PR 22-MAR-2001; 2001US-0277833P.  
 PR 23-MAR-2001; 2001US-0278152P.  
 PR 26-MAR-2001; 2001US-0278894P.  
 PR 27-MAR-2001; 2001US-0278999P.  
 PR 27-MAR-2001; 2001US-0279036P.  
 PR 27-MAR-2001; 2001US-0279344P.  
 PR 30-MAR-2001; 2001US-0279733P.  
 PR 30-MAR-2001; 2001US-027995P.  
 PR 02-APR-2001; 2001US-0280233P.  
 PR 02-APR-2001; 2001US-0280802P.  
 PR 02-APR-2001; 2001US-0280822P.  
 PR 04-APR-2001; 2001US-0280900P.  
 PR 13-APR-2001; 2001US-028575P.  
 PR 30-APR-2001; 2001US-0287424P.  
 PR 02-MAY-2001; 2001US-0288066P.  
 PR 03-MAY-2001; 2001US-0288342P.  
 PR 15-MAY-2001; 2001US-0291190P.  
 PR 16-MAY-2001; 2001US-0291099P.  
 PR 16-MAY-2001; 2001US-029140P.  
 PR 30-MAY-2001; 2001US-0294885P.  
 PR 31-MAY-2001; 2001US-0294899P.  
 PR 19-JUN-2001; 2001US-029903P.  
 PR 18-JUN-2001; 2001US-029903P.  
 PR 10-JUL-2001; 2001US-0304354P.  
 PR 31-JUL-2001; 2001US-0309198P.  
 PR 16-AUG-2001; 2001US-0312903P.  
 PR 10-SEP-2001; 2001US-0318422P.  
 PR 12-SEP-2001; 2001US-0318770P.  
 PR 27-SEP-2001; 2001US-0325430P.

PR 27-SEP-2001; 2001US-0325681P.  
 PR 18-OCT-2001; 2001US-0330580P.  
 PR 31-OCT-2001; 2001US-0335301P.  
 PR 14-NOV-2001; 2001US-0332172P.  
 PR 14-NOV-2001; 2001US-0332211P.  
 PR 14-NOV-2001; 2001US-0333184P.  
 PR 14-NOV-2001; 2001US-0333212P.  
 PR 21-NOV-2001; 2001US-0332094P.  
 PR 03-DEC-2001; 2001US-0338092P.  
 PR 04-DEC-2001; 2001US-0337785P.  
 PR 03-JAN-2002; 2002US-0345705P.  
 PR 07-MAR-2002; 2002US-0009290.

XX PA (CURA-) CURAGEN CORP.  
 XX PR Padigaru M, Spyrek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L; PT Zarhusen BD, Guiev V, Ji W, Gorman L, Miller CE, Kekuda R; PT Paturrajan M, Gangoli E, Vernet CM, Guo X, Tchernev V; PT Fernandes ER, Caaman SJ, Malvankar UM, Gerlach V, Liu Y, Anderson D; PT Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP; PT Lepley DM, Rieger DK; DR WPI; 2002-723332/78.  
 XX DR N-PSDB; ABX97178.

PT NOVX polypeptides and poly nucleotides, useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g., cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma.

XX PS Claim 1, Page 461, 1103pp; English.

XX This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABU65011-ABU65218 represent the NOVX polypeptides encoded by CC ABX97008-ABX97185

XX Sequence 683 AA;

Query Match, Best Local Similarity 100.0%; Score 725; DB 5; Length 683;  
 Matches 137; Consistency 100.0%; Pre. No. 5, 8e-74; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTKERYMOMRETMSSTSTLGFRIGKIKRADGTCTNFKKTQALEQVTKYLEDVGDGV 60  
 Db 531 AVTKERYMOMRETMSSTSTLGFRIGKIKRADGTCTNFKKTQALEQVTKYLEDVGDGV 590

QY 61 ILQKQVACLEBLREALIESPPKTHEVWSSLFLVHDHGGLAKYMMIDGKTVVALPDR 120  
 Db 591 ILQKQVACLEBLREALIESPPKTHEVWSSLFLVHDHGGLAKYMMIDGKTVVALPDR 650

QY 121 LSHRLPWAEGNRDGYL 137  
 Db 651 LSHRLPWAEGNRDGYL 667

**RESULT 6**  
 ID ADN62073  
 AC ADN62073 standard; protein; 683 AA.  
 XX DT 01-JUL-2004 (first entry)  
 XX DE Human novel protein NOV123a.

KW Human; NOX; diabetes; obesity; infectious disease; anorexia; PR 04-DEC-2001; 2001US-03337185P.  
 KW cancer-associated cachexia; cancer; neurodegenerative disorder; PR 03-JAN-2002; 2002US-0345705P.  
 KW Alzheimer's disease; Parkinson's disease; immune disorder; XX (PADI) PADIGARU M.  
 KW haematopoietic disorder; dyslipidaemia; chronic disease. XX (SPYTC) SPYTEK K A.  
 OS Homo sapiens. XX (SHEN) SHENOY S G.  
 XX US2004043382-A1. XX (TAUP) TAUPIER R J.  
 XX PD 04-MAR-2004. XX (PENA) PENA C E A.  
 XX PR 07-MAR-2002; 2002US-00092900. XX (LILI) LI L.  
 XX PR 08-MAR-2001; 2001US-0274191P. XX (ZERH) ZERHUSEN B D.  
 XX PR 08-MAR-2001; 2001US-0274194P. XX (GUSEV) GUSEV V Y.  
 XX PR 08-MAR-2001; 2001US-0274281. XX (JIMW) JI W.  
 XX PR 08-MAR-2001; 2001US-0274222P. XX (GORM) GORMAN L.  
 XX PR 09-MAR-2001; 2001US-0274499P. XX (MILL) MILLER C E.  
 XX PR 12-MAR-2001; 2001US-0275235P. XX (KEKU) KEKUDA R.  
 XX PR 13-MAR-2001; 2001US-0275578P. XX (PATT) PATTURAJAN M.  
 XX PR 13-MAR-2001; 2001US-0275579P. XX (GANG) GANGOLLI E A.  
 XX PR 14-MAR-2001; 2001US-0275601P. XX (VERN) VERNET C A M.  
 XX PR 14-MAR-2001; 2001US-0276000P. XX (GUOX) GUO X S.  
 XX PR 16-MAR-2001; 2001US-0276776P. XX (TCHB) TCHERNEV V T.  
 XX PR 19-MAR-2001; 2001US-0276994P. XX (SPAD) SPADRA S K.  
 XX PR 20-MAR-2001; 2001US-0277239P. XX (FERN) FERNANDES E R.  
 XX PR 20-MAR-2001; 2001US-0277327P. XX (CASM) CASMAN S J.  
 XX PR 20-MAR-2001; 2001US-0277338P. XX (MALY) MALYANTAR U M.  
 XX PR 21-MAR-2001; 2001US-0277791P. XX (GERI) GERLACH V.  
 XX PR 22-MAR-2001; 2001US-0277833P. XX (LIU) LIU Y.  
 XX PR 23-MAR-2001; 2001US-0278152P. XX (ANDR) ANDERSON D W.  
 XX PR 26-MAR-2001; 2001US-0278894P. XX (PA) PA  
 XX PR 27-MAR-2001; 2001US-0278999P. XX (CATT) CATTERTON E.  
 XX PR 27-MAR-2001; 2001US-0279036P. XX (LEIT) LEITE M W.  
 XX PR 28-MAR-2001; 2001US-0279344P. XX (ZHON) ZHONG H.  
 XX PR 30-MAR-2001; 2001US-0279995P. XX (ALSO) ALSOBRICK J P.  
 XX PR 30-MAR-2001; 2001US-0280233P. XX (LEPU) LEPLEY D M.  
 XX PR 02-APR-2001; 2001US-0280802P. XX (RIEG) RIEGER D K.  
 XX PR 02-APR-2001; 2001US-0280900P. XX (BURG) BURGESS C E.  
 XX PR 04-APR-2001; 2001US-0281444P. XX (DR) DR  
 XX PR 13-APR-2001; 2001US-0283675P. XX (WPI) WPI; 2004-225593/21.  
 XX PR 30-APR-2001; 2001US-0287424P. XX (N-PSDB) N-PSDB; ADN62072.  
 XX PR 02-MAY-2001; 2001US-0289066P.  
 XX PR 03-MAY-2001; 2001US-0289342P.  
 XX PR 03-MAY-2001; 2001US-0288528P.  
 XX PR 15-MAY-2001; 2001US-0291190P.  
 XX PR 15-MAY-2001; 2001US-0291240P.  
 XX PR 16-MAY-2001; 2001US-0294485P.  
 XX PR 30-MAY-2001; 2001US-0294889P.  
 XX PR 31-MAY-2001; 2001US-0295027P.  
 XX PR 31-MAY-2001; 2001US-0294999P.  
 XX PR 18-JUN-2001; 2001US-0295310P.  
 XX PR 19-JUN-2001; 2001US-0299310P.  
 XX PR 10-JUL-2001; 2001US-0303545P.  
 XX PR 31-JUL-2001; 2001US-0309198P.  
 XX PR 15-AUG-2001; 2001US-0312903P.  
 XX PR 10-SEP-2001; 2001US-0318462P.  
 XX PR 12-SEP-2001; 2001US-0318770P.  
 XX PR 27-SEP-2001; 2001US-0325430P.  
 XX PR 18-OCT-2001; 2001US-0325681P.  
 XX PR 31-OCT-2001; 2001US-0335301P.  
 XX PR 14-NOV-2001; 2001US-0332172P.  
 XX PR 14-NOV-2001; 2001US-0332271P.  
 XX PR 14-NOV-2001; 2001US-0332272P.  
 XX PR 14-NOV-2001; 2001US-0331848P.  
 XX PR 14-NOV-2001; 2001US-0333272P.  
 XX PR 21-NOV-2001; 2001US-0332094P.  
 XX PR 03-DEC-2001; 2001US-0337426P.  
 XX PR 03-DEC-2001; 2001US-0338092P.

The invention relates to an isolated polypeptide (designated NOX<sup>+</sup>, or NOV<sup>+</sup>NOV127) comprising a sequence selected from 178 fully defined amino acid sequences (and their mature forms, variants and fragments). Also included are an isolated nucleic acid molecule encoding NOX<sup>+</sup>, a vector comprising the nucleic acid, a cell comprising the vector, methods for determining the presence or amount of the polypeptide or the nucleic acid molecule in a sample, methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject, a method for identifying an agent that binds to the above polypeptide, a method for identifying a potential therapeutic agent for use in the treatment of a pathology that is related to aberrant expression or physiological interactions of the polypeptide, a method of screening for a modulator of activity or of latency or pre-disposition to a pathology associated with the polypeptide and a method for modulating the activity of the polypeptide cited above. The composition and methods are useful for diagnosing, preventing or treating diseases such as diabetes, obesity, infectious diseases, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or Parkinson's disease, haematopoietic like disorders, dyslipidaemias, and other chronic diseases. These may also be used in

CC	chromosome mapping, tissue typing, preventive medicine and
CC	pharmacogenomics. The polypeptides are also useful as vaccines. The
CC	present sequence represents a NovX protein of the invention.
CC	SQ
Sequence 683 AA;	
RESULT 7	100.0%; Score 725; DB 8; Length 683;
ID AEB87638	Best Local Similarity 100.0%; Pred. No. 5. 74%; O; Bimatches 137; Conservative 0; Mismatches 0; Index 0; Caps
XX	Matches 137; Conservative 0; Mismatches 0; Index 0; Caps
AC AEB87638;	
XX	
DT 20-OCT-2005 (first entry)	
XX	
DE Human inositol-trisphosphate 3-kinase C (ITPKC).	
XX	
KW Inositol-trisphosphate 3-kinase C; ITPKC; insulin-like growth factor receptor modulator; cytoblastic; cancer;	
KW neoplasm; gene therapy; antisense therapy; antibody therapy; drug screening; diagnosis; enzyme.	
KW	
XX	
OS Homo sapiens.	
XX	
PH	
FT Key	Location/Qualifiers
FT Domain	393 .. 678
FT	/note= "Inositol Polyphosphate kinase domain"
XX	
PN WO2005072475-A2.	
XX	
PD 11-AUG-2005.	
XX	
PF 27-JAN-2005; 2005WO-US003560.	
PR 28-JAN-2004; 2004US-0539837P.	
XX	
PA (EXBL-) EXELIXIS INC.	
XX	
PI Friedman L, Francis-Lang H, Parks AL, Shaw KJ, Bjerke LM;	
PI Heuer TS;	
XX	
DR WPI; 2005-555620/56.	
DR N-PDB; ABB87639.	
DR RESEQ; NP_076470.	
XX	
PT Identifying candidate Insulin Growth Factor Receptor pathway modulating agents useful for diagnosing or treating, for e.g. cancer, comprises screening for agents that modulate the activity of Inositol 1,4,5-triphosphate 3-kinase.	
PT	
PS Disclosure; SEQ ID NO 10; 87DP; English.	
XX	
CC The present sequence is the protein sequence of human inositol-trisphosphate 3-kinase C (ITPKC). A dominant loss of function screening was carried out in <i>Drosophila</i> to identify genes that interact with or modulate the insulin-like growth factor receptor (IGFR) signaling pathway. Modifiers of the IGFR pathway were isolated, and the human triphosphate 3-kinase.	
CC	

orthologs of these modifiers were identified as ITPKs. The invention provides methods for using these IGFIR modifier genes and polypeptides to identify ITPK-modulating agents that are candidate therapeutic agents for use in the treatment of disorders associated with defective or impaired IGFIR function and/or ITPK function. In one embodiment, candidate ITPK modulator agents are tested in an assay system comprising an ITPK polypeptide or nucleic acid. Agents that produce a change in the activity of the assay system relative to controls are identified as candidate IGFIR modulating agents. The screening assay system may be a binding assay, an apoptosis assay, a cell proliferation assay, an angiogenesis assay or a hypoxic induction assay. Preferred ITPK-modulating agents include small molecule modulators, nucleic acid molecules such as antisense oligomers or phosphorothioate morpholino oligomers, and antibodies. A probe for ITPK expression is used in a claimed method for diagnosing a disease, particularly cancer.

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
 PI Zhou P, Goodrich R, Drmanac RT;  
 XX DR WPI: 2001-442253/47.  
 DR N-PSDB; AAI60549.

PT Novel nucleic acids and polypeptides, useful for treating disorders such  
 AB central nervous system injuries.  
 XX PS Example 2; SEQ ID NO 6324; 10078PP; English.

CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
 encoded polypeptides (AAM18642-AAM2213) with nootropic,  
 immunosuppressant and cycostatic activity. The polynucleotides are useful  
 in gene therapy. A composition containing a polypeptide or polynucleotide  
 of the invention may be used to treat diseases of the peripheral nervous  
 system, such as peripheral nervous injuries, peripheral neuropathy and  
 localised neuropathies and central nervous system diseases, such as  
 Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 utilisation of the activities such as: Immune system suppression,  
 Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 C.N.S disorders. Note: The sequence data for this patent did not form  
 part of the printed specification

CC Sequence 687 AA;

Query Match 100.0%; Score 725; DB 4; Length 687;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVTKPRMQRMTMSSTSTLGRIGKIKAGTCTNPKQALEQTKVLEDFVGDHV 60  
 Db 535 AVTKPRMQRMTMSSTSTLGRIGKIKAGTCTNPKQALEQTKVLEDFVGDHV 594

Qy 61 ILQKVYACLEIRALEISPFKTHEVGSSLFLVADHTGIAKVMMDFGKVALPDHQ 120  
 Db 595 ILQKVYACLEIRALEISPFKTHEVGSSLFLVADHTGIAKVMMDFGKVALPDHQ 654

Db 655 LSHRLPWAEGNRGREDGYL 671

RESULT 9  
 AAM39607  
 ID AAM39607 standard; protein; 711 AA.  
 AC AAM39607;  
 XX DT 22-OCT-2001 (first entry)  
 XX DB Human polypeptide SEQ ID NO 2752.

XX Human; nootropic; immunosuppressant; cycostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukemia.  
 XX OS Homo sapiens.  
 XX PN WO200153312-A1.

PD 26-JUL-2001.  
 XX PP 26-DEC-2000; 2000WO-US034263.  
 XX PR 23-DEC-1999; 99US-00471275.  
 PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.  
 PR 20-JUN-2000; 2000US-00598042.  
 PR 19-JUL-2001; 2000US-00620112.  
 PR 03-AUG-2000; 2000US-00653450.  
 PR 14-SEP-2000; 2000US-00662191.  
 PR 19-OCT-2000; 2000US-00693036.  
 PR 29-NOV-2000; 2000US-00727344.

PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
 PI Zhou P, Goodrich R, Drmanac RT;  
 XX DR WPI: 2001-442253/47.  
 DR N-PSDB; AAI58763.

PT Novel nucleic acids and polypeptides, useful for treating disorders such  
 AB central nervous system injuries.  
 XX PS Example 4; SEQ ID NO 2752; 10078PP; English.

CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
 encoded polypeptides (AAM18642-AAM2213) with nootropic,  
 immunosuppressant and cycostatic activity. The polynucleotides are useful  
 in gene therapy. A composition containing a polypeptide or polynucleotide  
 of the invention may be used to treat diseases of the peripheral nervous  
 system, such as peripheral nervous injuries, peripheral neuropathy and  
 localised neuropathies and central nervous system diseases, such as  
 Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 utilisation of the activities such as: Immune system suppression,  
 Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 C.N.S disorders. Note: The sequence data for this patent did not form  
 part of the printed specification

CC Sequence 711 AA;

Query Match 100.0%; Score 725; DB 4; Length 711;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVTKPRMQRMTMSSTSTLGRIGKIKAGTCTNPKQALEQTKVLEDFVGDHV 60  
 Db 559 AVTKPRMQRMTMSSTSTLGRIGKIKAGTCTNPKQALEQTKVLEDFVGDHV 618

Qy 61 ILQKVYACLEIRALEISPFKTHEVGSSLFLVADHTGIAKVMMDFGKVALPDHQ 120  
 Db 619 ILQKVYACLEIRALEISPFKTHEVGSSLFLVADHTGIAKVMMDFGKVALPDHQ 678

Qy 121 LSHRLPWAEGNRGREDGYL 137  
 Db 679 LSHRLPWAEGNRGREDGYL 695

RESULT 10  
 ABB09772  
 ID ABB09772 standard; protein; 461 AA.  
 XX AC ABB09772;  
 XX DT 22-JUL-2002 (first entry)  
 XX DE Amino acid sequence of human inositol-1,4,5-triphosphate 3 kinase-A.  
 XX IP3 kinase; inositol-1,4,5-triphosphate kinase; enzyme; oxidative stress;  
 KW endoplasmic reticulum stress; neurodegeneration; retina; free radical;  
 KW chronic infection; arthritis; cancer; cystic fibrosis;  
 KW Alzheimer's disease; Huntington's disease; pigmentary retinopathy;  
 KW DIP3K1; DIP3K2.

OS Homo sapiens.  
 XX  
 PN FR2813612-A1.  
 XX  
 PD 08-MAR-2002.  
 XX  
 PF 07-SEP-2000; 2000FR-00011397.  
 XX  
 PR 07-SEP-2000; 2000FR-00011397.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Tricoire H, Monnier V, Pret AM, Cabet DE, Brisard J, Vandurka P;  
 PI Giardot F;  
 XX  
 DR WPI; 2002-260343/31.  
 DR N-PSDB; ABL56444.  
 XX  
 PT New Proteins with inositol-triphosphate kinase activity, useful e.g. for  
 PT treating oxidative stress and neurodegeneration.  
 XX  
 PS Claim 4; Fig 3; 69pp; French.  
 XX  
 CC The present sequence represents inositol-1,4,5-triphosphate 3 (IP3)  
 CC kinase-A protein. The specification also describes Drosophila IP3 kinase  
 CC proteins, designated dIP3K1 and dIP3K2. This protein has IP3/inositol-  
 CC 1,4,5-triphosphate kinase activity. The specification describes the use  
 CC of IP3 kinase proteins to prepare compositions for treating diseases  
 CC associated with oxidative stress, stress of the endoplasmic reticulum or  
 CC neurodegeneration, particularly of the retina. Overexpression of IP3  
 CC kinase protects cells against the damaging effects of free radicals  
 CC without altering free radical homeostasis within the cell. The IP3  
 CC proteins are used for treating disorders associated with oxidative  
 CC stress, stress on the endoplasmic reticulum and neurodegeneration,  
 CC particularly chronic infection (such as arthritis and some forms of  
 CC cancer); cystic fibrosis; Alzheimer's and Huntington's diseases, and  
 CC pigmentary retinopathy. Transgenic animals that lack the gene for IP3  
 CC kinase proteins are used to identify phenotypic alterations associated  
 CC with loss of this gene  
 XX  
 Sequence 461 AA;

Query Match 69.5%; Score 504; DB 5; Length 461;  
 Best Local Similarity 66.4%; Pred. No. 9.4e-49;  
 Matches 91; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 1 AVTKERYMQRRETMSSTSTGFRIGKKGADGTNPKTKTQALQVTKVLEDFVGDHV 60  
 DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 309 AVTKPYRQMQRREGSSTTGFRRIGKKGADGSCTDFKTRRSRQEVLVFEFVQGDEE 368  
 QY 61 ILQKTYVACELBELREALBISPPFKTHEVVGSSLLFVHDHTGLAKVMMIDFGKTVALPDHQ 120  
 DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 369 VLRYYRLQQLQDIRDTEVSFFRHEVIGSSLLFVHDCHAGVWLFQDFGKTTPLDQI 428  
 QY 121 LSHRPWAEGRREDGIL 137  
 DB 429 LDHRRPWEEGNRREDGIL 445  
 RESULT 11  
 ID ADD44008  
 XX ADD44008 standard; protein; 461 AA.  
 AC  
 DT 15-JUL-2004 (first entry)  
 XX  
 XX  
 DE Amino acid sequence of human 1D-MYO-inositol triphosphate 3 kinase A.  
 XX  
 KW protein complex; neurological disease; stroke; neurodegeneration;  
 KW Wallerian degeneration; Alzheimer's disease; neurological disorder;  
 KW epilepsy; inflammatory condition; ulcerative colitis; Crohn's disease;  
 KW atherosclerosis; 1D-MYO-Inositol triphosphate 3 kinase A; ASK1; ASK2;  
 KW  
 KW ASK3; CAMKII beta; CAMKII delta; CAMKII gamma; casein kinase II alpha;  
 KW Cdc37; CHK2; CTCL tumour antigen SE20-4; EF-1 alpha 1; ENaP;  
 KW FLU14653 NT2RP2002252; FLUJ0839 FEBR2002429; HERC2;  
 KW inositol polyphosphate-5-phosphatase; inositol-1,4,5-triphosphate kinase type 1; IRAK1; IRAK4; KIAA1441; MSTP030;  
 KW Nek3; PAR3; Pellino 1; Pellino 3; podocalyxin-like protein 1 precursor;  
 KW Pushover; S-adenosylhomocysteine; secretory carrier-associated membrane protein 2; surfeit locus protein 2;  
 KW ubiquitin carboxyl terminal hydrolase 11; upsteam regulatory element binding protein 1; Vartul;  
 KW Werner's syndrome helicase interacting protein; WHIP;  
 KW X-ray repair cross complementing protein 4.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004031242-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 11-SEP-2003; 2003WO-EP010110.  
 XX  
 PR 12-SEP-2002; 2002EP-00020495.  
 PR 12-SEP-2002; 2002EP-0002496.  
 PR 12-SEP-2002; 2002EP-00020497.  
 XX  
 PA (CELL-) CELLZONE AG.  
 XX  
 PI Bouwmeester T, Drewes G, Jackson D, Helftenbein G, Schirle M;  
 PI Kuester B, Hof C;  
 XX  
 DR WPI; 2004-316467/29.  
 XX  
 PT New complex comprising at least one first protein, and at least one  
 PT second protein, useful for treating stroke, Alzheimer's disease,  
 PT neurological disorders such as epilepsy, and inflammatory conditions such  
 PT as ulcerative colitis.  
 XX  
 PS Example; Page 243-245; 287pp; English.  
 XX  
 CC The specification describes protein complexes involved in cellular  
 CC processes which have been shown to be critical for the development of  
 CC various forms of neurological diseases. Three protein complexes were  
 CC identified: ASK2 protein complex. The protein complex are useful for treating diseases and  
 CC protein complex. The protein complex are useful for treating diseases and  
 CC disorders, e.g. stroke, neurodegeneration such as Wallerian degeneration,  
 CC Alzheimer's disease, neurological disorders such as epilepsy, and  
 CC inflammatory disorders such as ulcerative colitis, Crohn's disease or  
 CC atherosclerosis. Proteins identified as being part of the protein  
 CC complexes of the invention are 1D-MYO-inositol triphosphate 3 kinase A,  
 CC ASK1, ASK2, ASK3, CAMKII beta, CAMKII gamma, casein kinase  
 II alpha, Cdc37, CHK2, CTCL tumour antigen SE20-4, EF-1 alpha 1, ENaP,  
 CC FLUJ4653 NT2RP2002252; FLUJ0839 FEBR2002429; HERC2, two hypothetical  
 CC proteins of 35.5 kDa and 49.3 kDa, inositol polyphosphate-5-phosphatase,  
 CC inositol-1,4,5-triphosphate kinase type 1, IRAK1, IRAK4, KIAA1441,  
 CC MSTP030, Nek3, PAR3, Pellino 1, Pellino 3, podocalyxin-like protein 1  
 CC precursor, Pushover, a putative S-adenosylhomocysteine; secretory  
 CC carrier-associated membrane protein 2, surfeit locus protein 2, ubiquitin  
 CC carboxyl terminal hydrolase 11, upsteam regulatory element binding  
 CC protein 1, Vartul, Werner's syndrome helicase interacting protein (WHIP),  
 CC X-ray repair cross complementing protein 4 (isform 1). The present  
 CC sequence represents 1D-MYO-inositol triphosphate 3 kinase A.  
 XX  
 Sequence 461 AA;

Query Match 69.5%; Score 504; DB 8; Length 461;  
 Best Local Similarity 66.4%; Pred. No. 9.4e-49;  
 Matches 91; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 1 AVTKERYMQRRETMSSTSTGFRIGKKGADGTNPKTKTQALQVTKVLEDFVGDHV 60  
 DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 309 AVTKPYRQMQRREGSSTTGFRRIGKKGADGSCTDFKTRRSRQEVLVFEFVQGDEE 368  
 QY 61 ILQKTYVACELBELREALBISPPFKTHEVVGSSLLFVHDHTGLAKVMMIDFGKTVALPDHQ 120



CC pigmentary retinopathy. Transgenic animals that lack the gene for IP3 kinase proteins are used to identify phenotypic alterations associated with loss of this gene

SQ Sequence 472 AA;

Query Match 68.0%; Score 493; DB 5; Length 472;

Best Local Similarity 67.9%; Pred. No. 1: 8e-4730; Indels 0; Gaps 0;

Matches 93; Conservative 14; Mismatches 3; Insertions 0;

QY 1 AVTKPRIMQWRETMSSSTLGPRIEGIKKADGCTNINKTQALEQVTKULEFDVDDH 60

Db 316 AVTKPRIMQWRETMSSSTLGPRIEGIKKADGCTNINKTQALEQVTKULEFDVDDH 375

QY 61 ILOKVKVACELRELAEELSPPFKTHEVVGSSLFVHDINGLAKWMMDPFGKTVALPHOT 120

Db 376 ILIAYRDRLLKAIRTLEVSPPFKCHEVIGQSSLFLHDKEQAKVWMDPFGKTVPLPEQ 435

Qy 121 LSHRLPWAENREGCYL 137

Db 436 LQHDVVPWQEGNRDGYL 452

RESULT 15

ID ABB09783

ID ABB09783 standard; protein; 472 AA.

XX ABB09783;

XX

DT 22-JUL-2002 (first entry)

XX

DE Amino acid sequence of human inositol-1,4,5-triphosphate 3 kinase-B.

XX

KW IP3 kinase; inositol-1,4,5-triphosphate kinase; enzyme; oxidative stress; endoplasmic reticulum stress; neurodegeneration; retina; free radical; chronic infection; arthritis; cancer; cystic fibrosis; Alzheimer's disease; Huntington's disease; pigmentary retinopathy; DIP3K1; DIP3K2.

XX

KW Homo sapiens.

OS Homo sapiens.

XX

PN WO20020742-A1.

XX

PD 14-MAR-2002.

XX

PF 31-AUG-2001; 2001WO-FR002708.

XX

PR 07-SEP-2000; 2000FR-00011397.

XX

PA (CNRS ) CENT NAT RECH SCI.

XX

PI Tricocire H, Monnier V, Pret A, Busson DE, Zahraoui J, Vandurka P;

PI Girardot F;

XX

DR WPI; 2002-260343/31.

XX

PT New proteins with inositol-triphosphate kinase activity, useful e.g. for treating oxidative stress and neurodegeneration.

XX

PS Claim 4; Page 54-55; 64PP; French.

CC The present sequence represents inositol-1,4,5-triphosphate 3 (IP3) kinase-B protein. The specification also describes Drosophila IP3 kinase proteins, designated DIP3K1 and DIP3K2. This protein has IP3 (inositol-1,4,5-triphosphate) kinase activity. The specification describes the use of IP3 kinase proteins to prepare compositions for treating diseases associated with oxidative stress, stress of the endoplasmic reticulum or neurodegeneration, particularly of the retina. Overexpression of IP3 kinase protects cells against the damaging effects of free radicals without altering free radical homeostasis within the cell. The IP3 proteins are used for treating disorders associated with oxidative stress, stress on the endoplasmic reticulum and neurodegeneration, particularly chronic infection (such as arthritis and some forms of

CC cancer); cystic fibrosis; Alzheimer's and Huntington's diseases, and  
 CC pigmentary retinopathy. Transgenic animals that lack the gene for IP3  
 CC kinase proteins are used to identify phenotypic alterations associated  
 CC with loss of this gene. This specification is equivalent to FR2813612  
 XX

SQ Sequence 472 AA;

Query Match 68.0%; Score 493; DB 5; length 472;  
 Best Local Similarity 67.9%; Pred. No. 1. 8e-47; Matches 93; Conservative 14; Mismatches 30; Indels 0; Gaps 0;  
 QY 1 AVTKPRYMQWBTMSSSTLAFRIGIIGKKAQGTCNTNFKKTOALBVTKVLEDFYQGDHV 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 316 AVTKPRYMQWBTMSSSTLAFRIGIIGKKAQGTCNTNFKKTOALBVTKVLEDFYQGDHV 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 QY 61 ILOKVYACLERLREALRISPFKTHKVGSSLFVFDHTGIAKUWMDGCTVALPDHQT 120  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 376 IILAYVDRKLKIRTLEVSPPFKCHSYTGSILFLIDKKBQAKUWMDGCTPAPEGQT 435  
 |||||:|||||:|||||:|||||:|||||:|||||:  
 QY 121 LSHRLPWAEGREDGYL 137  
 |||||:|||||:  
 Db 436 IQHDVWPWQEGNREDGYL 452

Search completed: May 21, 2006, 04:20:23  
 Job time : 196 sec

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GenCore version 5.1.8

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OM protein - protein search, using sw model

Run on:

May 21, 2006, 04:20:44 ; Search time 38 Seconds

(Without alignments) 346.887 Million cell updates/sec

Title: US-10-781-581-226  
Perfect score: 725  
Sequence: 1 AVTKPRMWMQWRETMSSSTL.....HQLTSHRLPWAEGNREDDGYL 137Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.0\*

1: pir1:\*2: pir2:\*3: pir3:\*4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	506	69.8	459	2	S13064		1D-myo-inositol-triaphosphate 3-kinase (EC 2.7.1.127) A - rat
2	504	69.5	461	2	JN0129		N;Alternate names: inositol-1,4,5-triaphosphate 3-kinase
3	493	68.0	472	2	SL7680		C;Species: Rattus norvegicus (Norway rat)
4	493	68.0	946	2	JCT7810		C;Date: 21-Nov-1993 #sequence revision 10-Nov-1995#text_change 09-Jul-2004
5	487	67.2	673	2	S41053		C;Accession: S13064; A34854; S56747
6	321	44.3	394	2	T42512		R;Takazawa, K.; Vandekerckhove, J.; Dumont, J.E.; Ernoux, C.
7	321	44.3	461	2	T42513		Biochem. J. 310, 109-115, 1995
8	321	44.3	486	2	T25639		A;Title: Active site labelling of inositol 1,4,5-triaphosphate 3-kinase A by phenylglyoxal
9	321	44.3	494	2	T42444		A;Reference number: S56747; MUID:95374430; PMID:7646431
10	124	268	2	T52024		A;Accession: S56747	
11	78	10.8	555	2	T32105		A;Molecule type: protein
12	77.5	10.7	476	2	T27707		A;Residues: 315-325 <TAK>
13	77.5	10.7	775	2	B70320		A;Cross-references: UNIPARC:UPI00001679B7; GB:MB29787; NID:9204987; PIDN:AA41457.1; PID: A;Experimental source: brain
14	76	10.5	1047	2	AT2002		C;Function: A;Description: catalyzes the phosphorylation of inositol 1,4,5-triaphosphate 3-kinase A by phenylglyoxal
15	75	10.3	302	2	H86391		A;Keywords: brain; phosphoprotein; phosphotransferase
16	74.5	10.3	238	2	A81422		F;119/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
17	74.5	10.3	922	2	AG1827		F;195/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
18	74	10.2	288	2	H90048		F;309/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #status predicted
19	74	10.2	912	2	T11961		F;46/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
20	73.5	10.1	361	2	AC1437		Query Match 69.8%; Score 506; DB 2; Length 459;
21	73.5	10.1	607	2	G84630		Best Local Similarity 69.8%; Pred. No. 3.3e-40; Matches 92; Conservative 22; Mismatches 23; Indels 0; Gaps 0;
22	73	10.1	356	2	C70398		QY 1 AVTKPRMWMQWRETMSSSTLFGRIEGIKKADGTCNTNFKTQLEQVYKLEPFDVGDHV 60
23	73	10.1	810	2	T45679		Db 307 AVTKPRMWMQWRETMSSSTLFGRIEGIKKADGTCNTNFKTQLEQVYKLEPFDVGDHV 66
24	72.5	10.0	349	2	A72750		27.5 62.5 10.0 362 2 A64212 2 D86903 2 T25848 2 T35760
25	72.5	10.0	362	2	A64212		61 ILQKVVACIIEELREALETSPPFKTHEVGSSLLFVHDITGLAKWVMDFGKTVLAPDQT 120
26	72.5	10.0	625	2	D86903		
27	72.5	9.9	467	2	T25848		
28	72	9.9	602	1	T35760		

DNA helicase relat  
leucyl-tRNA synthetase  
hypothetical protein  
cysteine protein  
hypothetical protein  
carboxypeptidase D  
spectrin beta chain  
aryl-alcohol dehydrogenase  
probable cytochrome  
env polyprotein  
env polyprotein  
probable b-zip trimer  
hypothetical protein  
outer membrane lipase  
endo-exonuclease Y  
gp70 protein - mur

## ALIGNMENTS

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.0\*

1: pir1:\*2: pir2:\*3: pir3:\*4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	506	69.8	459	2	S13064		1D-myo-inositol-triaphosphate 3-kinase (EC 2.7.1.127) A - rat
2	504	69.5	461	2	JN0129		N;Alternate names: inositol-1,4,5-triaphosphate 3-kinase
3	493	68.0	472	2	SL7680		C;Species: Rattus norvegicus (Norway rat)
4	493	68.0	946	2	JCT7810		C;Date: 21-Nov-1993 #sequence revision 10-Nov-1995#text_change 09-Jul-2004
5	487	67.2	673	2	S41053		R;Takazawa, K.; Vandekerckhove, J.; Dumont, J.E.; Ernoux, C.
6	321	44.3	394	2	T42512		Biochem. J. 310, 109-115, 1995
7	321	44.3	461	2	T42513		A;Title: Active site labelling of inositol 1,4,5-triaphosphate 3-kinase A by phenylglyoxal
8	321	44.3	486	2	T25639		A;Reference number: S56747; MUID:95374430; PMID:7646431
9	321	44.3	494	2	T42444		A;Accession: S56747
10	124	268	2	T50224		A;Molecule type: protein	
11	78	10.8	555	2	T32105		A;Residues: 315-325 <TAK>
12	77.5	10.7	476	2	T27707		A;Cross-references: UNIPARC:UPI0000179A9C
13	77.5	10.7	775	2	B70320		A;Experimental source: brain
14	76	10.5	1047	2	AT2002		C;Function: A;Description: catalyzes the phosphorylation of inositol 1,4,5-triaphosphate 3-kinase A by phenylglyoxal
15	75	10.3	302	2	H86391		A;Keywords: brain; phosphoprotein; phosphotransferase
16	74.5	10.3	238	2	A81422		F;119/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
17	74.5	10.3	922	2	AG1827		F;195/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
18	74	10.2	288	2	H87642		F;309/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #status predicted
19	74	10.2	912	2	T11961		F;46/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
20	73	10.1	361	2	AC1437		Query Match 69.8%; Score 506; DB 2; Length 459;
21	73.5	10.1	607	2	G84630		Best Local Similarity 69.8%; Pred. No. 3.3e-40; Matches 92; Conservative 22; Mismatches 23; Indels 0; Gaps 0;
22	73	10.1	356	2	C70398		QY 1 AVTKPRMWMQWRETMSSSTLFGRIEGIKKADGTCNTNFKTQLEQVYKLEPFDVGDHV 60
23	73	10.1	810	2	T45679		Db 307 AVTKPRMWMQWRETMSSSTLFGRIEGIKKADGTCNTNFKTQLEQVYKLEPFDVGDHV 66
24	72.5	10.0	349	2	A72750		27.5 62.5 10.0 362 2 A64212 2 D86903 2 T25848 2 T35760
25	72.5	10.0	362	2	A64212		61 ILQKVVACIIEELREALETSPPFKTHEVGSSLLFVHDITGLAKWVMDFGKTVLAPDQT 120
26	72.5	10.0	625	2	D86903		
27	72.5	9.9	467	2	T25848		
28	72	9.9	602	1	T35760		

Db	357 VLRVYVNLQQLQIRTLESDPFRRHEVWGSLLPTVHDKHRAGWVWLDGKTRPDRGQI 425
Qy	121 LSHRLPWAEGNRREDGYL 137
Db	427 LDHRRPWEEGNRREDGYL 443
RESULT 2	
JN0129	1D-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) A - human
N	Alternate names: inositol-1,4,5-trisphosphate 3-kinase A
C	Species: Homo sapiens (man)
C	Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C	Accession: JN0129; S13559
R	Takazawa, K.; Perret, J.; Dumont, J. E.; Erneux, C.
Biochem. Biophys. Res. Commun. 174, 529-535, 1991	
A	Title: Molecular cloning and expression of a human brain inositol 1,4,5-trisphosphate A
A	Reference number: JN0129; MUID:9120380; PMID:1847047
A	Accession: JN0129
A	Molecule type: mRNA
A	Residues: 1-461 <TAK1>
A	Cross-references: UNIPARC:UPI23677; UNIPARC:UPI000049A1A; EMBL:X54938; NID:932104; PID:126663; OMIM:147521
A	Gene: GDB:ITPKA
A	Map position: 15q15.1-15q21.1
C	Function:
A	Description: catalyzes the phosphorylation of inositol-1,4,5-trisphosphate to inositol-1,4,5-trisphosphate 3-kinase
C	Keywords: phosphoprotein; phosphotransferase
F	1-21/Binding site: phosphate (Ser) (covalent) (by cAMP- and calmodulin-dependent kinase F197/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted F311/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #status predicted F348/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
Query Match	69 5%; Score 504; DB 2; Length 461;
Best Local Similarity	66 4%; Pred. No. 5.2e-40;
Matches	91; Conservative 22; Mismatches 24; Indels 0; Gaps 0;
Qy	1 AVTKRYMQMRETTMSSTIIGFRIGGIKKADGTCTNPKQIQLAQTVKLEDFVGDHV 60
Db	309 AVTKRYMQMRETTMSSTIIGFRIGGIKKADGTCTNPKQIQLAQTVKLEDFVGDHV 60
Qy	61 ILQKYYVACLEBLREALEISPPFKTHVVGSSLFLFDHDTGLAKVMMIDFGKTVALPDHQT 120
Db	369 VLRRYIARLQOIRDLEVESEFPRRHEVIGSSLFLFDHCHRAVGMIDFGKTVIPPDQI 428
Qy	121 LSHRLPWAEGNRREDGYL 137
Db	429 LDHRRPWEEGNRREDGYL 445
RESULT 3	SL7682
N	1D-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) B - human
C	Alternate names: inositol-1,4,5-trisphosphate 3-kinase B
C	Species: Homo sapiens (man)
C	Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
C	Accession: S17682
R	Takazawa, K.; Perret, J.; Dumont, J. E.; Erneux, C.
Biochem. J. 218, 883-886, 1991	
A	Title: Molecular cloning and expression of a new putative inositol 1,4,5-trisphosphate A
A	Reference number: S17645; MUID:9137854; PMID:1654894
A	Accession: S17682
RESULT 4	
JC7810	1D-myo-inositol-1,4,5-trisphosphate 3-kinase B - human
C	Species: Homo sapiens (man)
C	Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 03-Jun-2002
C	Accession: JC7810
R	Desvergne, V.; Roymans, D.; Moreau, C.; Erneux, C.
Biochem. Biophys. Res. Commun. 291, 400-405, 2002	
A	Title: Cloning and expression of a full-length cDNA encoding human inositol 1,4,5-tri
A	Reference number: JC7810; PMID:1184619; MUID:21835501
A	Contents: Frontal cortex
A	Accession: JC7810
A	Molecule type: mRNA
A	Residues: 1-946 <DEW>
A	Cross-references: UNIPARC:UPI00017CD41; GB:Y18024
C	Comment: This enzyme, an isoenzyme of inositol 1,4,5-trisphosphate (InsP3) 3-kinase, is of calcium homeostasis. This enzyme is particularly sensitive to Ca <sup>2+</sup> in the presence of
Query Match	68 0%; Score 493; DB 2; Length 946;
Best Local Similarity	67.9%; Pred. No. 1.3e-38;
Matches	93; Conservative 14; Mismatches 30; Indels 0; Gaps 0;
Qy	1 AVTKRYMQMRETTMSSTIIGFRIGGIKKADGTCTNPKQIQLAQTVKLEDFVGDHV 60
Db	790 AVTKRYMQMRETTMSSTIIGFRIGGIKKADGTCTNPKQIQLAQTVKLEDFVGDHV 60
Qy	61 ILQKYYVACLEBLREALEISPPFKTHVVGSSLFLFDHDTGLAKVMMIDFGKTVALPDHQT 120
Db	850 ILAYRDKLRAITLLEVSFPRRHEVIGSSLFLFDHCHRAVGMIDFGKTVIPPDQI 909
Qy	121 LSHRLPWAEGNRREDGYL 137
Db	910 LQHDVFWQEGNRREDGYL 926
RESULT 5	S41053
1D-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) B - rat	
N	Alternate names: IP(3) 3-kinase
C	Species: Rat norvegicus (Norway rat)
C	Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C	Accession: S11053; S54549; S35963
R	Thomas, S.; Brake, B.; Luzzio, J. P.; Stanley, K.; Banting, G.
Biochem. Biophys. Acta 1220, 219-222, 1994	
A	Title: Isolation and sequencing of a full length cDNA encoding a novel rat inositol 1,4,5-trisphosphate A
A	Reference number: S41053; MUID:9414619; PMID:8312365
A	Accession: S41053

A;Molecule type: mRNA  
 A;Residues: 1-673 <TH0>  
 A;Cross-references: UNIPROT:Q91XW1; UNIPARC:UPI0000167A55; EMBL:X74227; NID:9396428; PID:11305; #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
 A;Experimental source: Liver  
 R;Vanweyenberg, V.; Communi, D.; D Santos, C.S.; Erneux, C.  
 R;Bloch, M.; J. 305, 428-435, 1995  
 A;Title: Tissue- and cell-specific expression of Ins(1,4,5)P(3) 3-kinase isoenzymes.  
 A;Reference number: S54349; PMID:95194317; PMID:7887896  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-172; T<sup>1</sup> 174-673 <VAN>  
 A;Cross-references: UNIPARC:UPI000017C89D  
 A;Experimental source: thymus  
 C;Function:  
 A;Description: catalyzes the phosphorylation of inositol-1,4,5-triphosphate to inositol-1,4,5-trisphosphate  
 C;Keywords: phosphoprotein; phosphotransferase

Query Match 67.2%; Score 487; DB 2; Length 673;  
 Best Local Similarity 67.2%; Pred. No. 3.3e-38;  
 Matches 92; Conservative 15; Mismatches 30; Indels 0; Gaps 0;

QY 1 AVTKPERYMQMRETTMSSTGPRIGKKAQDGTCNTNFKKTOALEQVTKVLEDFVGDHV 60  
 Db 517 AVTKPERYMQMRETTMSSTGPRIGKKAQDGTCNTNFKKTOALEQVTKVLEDFVGDHV 576  
 QY 61 -ILOKVKVACELBLREALBISPFKTHEWVGSSLLFVHDHTGLAKVMMIDFGKTVALPDHQ 120  
 Db 577 ILLAVYDRDLKAIKRETELEVSPFFKCHEVIGSSLLFIDHKKEQAKVMMIDFGKTVPLPEGQT 636  
 QY 121 LSRSRILWAGENRREDGYL 137  
 Db 637 LQHDVVPWQEGNRREDGYL 653

RESULT 6  
 T42512  
 1D-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) isoform 2 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
 C;Accession: T42512  
 R;Clandinin, T.R.; DeModena, J.A.; Sternberg, P.W.  
 Cell 92, 523-533, 1998  
 A;Title: Inositol trisphosphate mediates a RAS-independent response to LET-23 receptor  
 A;Reference number: 222166; PMID:98150857; PMID:9491893  
 A;Accession: T42512  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-394 <CLA>  
 A;Cross-references: UNIPROT:045050; UNIPARC:UPI0000079EP2; EMBL:AF045612; NID:92898159;  
 C;Genetics:  
 A;Gene: LFE-2  
 C;Keywords: phosphoprotein; phosphotransferase

Query Match 44.3%; Score 321; DB 2; Length 461;  
 Best Local Similarity 48.6%; Pred. No. 1.1e-22;  
 Matches 67; Conservative 21; Mismatches 48; Indels 2; Gaps 2;

QY 1 AVTKPERYMQMRETTMSSTGPRIGKKAQDGTCNTNFKKTOALEQVTKVLEDFVGDHV 60  
 Db 286 AVTKPERYMQMRETTMSSTGPRIGKKAQDGTCNTNFKKTOALEQVTKVLEDFVGDHV 345  
 QY 61 -ILOKVKVACELBLREALBISPFKTHEWVGSSLLFVHDHTGLAKVMMIDFGKTVALPDHQ 119  
 Db 346 RVRQQLIERLKSRAKIEHSSPFNSHEVVGSSLLFVHD-TEKVGWMIDPAKSSPVNGR 404  
 QY 120 LSRSRILWAGENRREDGYL 137  
 Db 405 TLNHRRTWIPGNEDGYL 422

RESULT 6  
 T42512  
 1D-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) isoform 3 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C;Accession: T25639  
 R;Miller, N.; Bradshaw, H.; Wamsley, P.  
 submitted to the EMBL Data Library, February 1997  
 A;Description: The sequence of C. elegans cosmid C46H11.  
 A;Reference number: 220061  
 A;Accession: T25639  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-486 <MLI>  
 A;Cross-references: UNIPARC:UPI00001798B5; EMBL:U88314; PIDN:AA842358.1; GSPDB:GN00019;  
 A;Experimental source: strain Bristol N2; clone C46H11  
 A;Genetics:  
 A;Gene: C46H11.4  
 A;Map position: 1  
 A;Introns: 15/3; 190/1; 359/3

Query Match 44.3%; Score 321; DB 2; Length 486;  
 Best Local Similarity 48.6%; Pred. No. 1.2e-22;  
 Matches 67; Conservative 21; Mismatches 48; Indels 2; Gaps 2;

QY 1 AVTKPERYMQMRETTMSSTGPRIGKKAQDGTCNTNFKKTOALEQVTKVLEDFVGDHV 60  
 Db 219 AVTKPERYMQMRETTMSSTGPRIGKKAQDGTCNTNFKKTOALEQVTKVLEDFVGDHV 278  
 QY 61 -ILOKVKVACELBLREALBISPFKTHEWVGSSLLFVHDHTGLAKVMMIDFGKTVALPDHQ 119  
 Db 279 RVRQQLIERLKSRAKIEHSSPFNSHEVVGSSLLFVHD-TEKVGWMIDPAKSSPVNGR 337  
 QY 120 LSRSRILWAGENRREDGYL 137  
 Db 338 TLNHRRTWIPGNEDGYL 355

RESULT 7  
 T42513  
 1D-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) isoform 3 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
 C;Accession: T42513  
 R;Clandinin, T.R.; DeModena, J.A.; Sternberg, P.W.  
 Cell 92, 523-533, 1998  
 A;Title: Inositol trisphosphate mediates a RAS-independent response to LET-23 receptor  
 A;Reference number: 222166; PMID:98150857; PMID:9491893  
 A;Accession: T42513  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-61 <CLA>  
 A;Cross-references: UNIPROT:045051; UNIPARC:UPI000008137D; EMBL:AF045613; NID:92898161;  
 A;Experimental source: strain Bristol N2; clone C46H11  
 A;Genetics:  
 A;Gene: LFE-2  
 C;Keywords: phosphoprotein; phosphotransferase

Query Match 44.3%; Score 321; DB 2; Length 461;  
 Best Local Similarity 48.6%; Pred. No. 1.1e-22;  
 Matches 67; Conservative 21; Mismatches 48; Indels 2; Gaps 2;

QY 1 AVTKPERYMQMRETTMSSTGPRIGKKAQDGTCNTNFKKTOALEQVTKVLEDFVGDHV 60  
 Db 286 AVTKPERYMQMRETTMSSTGPRIGKKAQDGTCNTNFKKTOALEQVTKVLEDFVGDHV 345  
 QY 61 -ILOKVKVACELBLREALBISPFKTHEWVGSSLLFVHDHTGLAKVMMIDFGKTVALPDHQ 119  
 Db 346 RVRQQLIERLKSRAKIEHSSPFNSHEVVGSSLLFVHD-TEKVGWMIDPAKSSPVNGR 404  
 QY 120 LSRSRILWAGENRREDGYL 137  
 Db 451 TLNHRRTWIPGNEDGYL 468

RESULT 9  
 T42513  
 1D-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) isoform 3 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C;Accession: T25639  
 R;Miller, N.; Bradshaw, H.; Wamsley, P.  
 submitted to the EMBL Data Library, February 1997  
 A;Description: The sequence of C. elegans cosmid C46H11.  
 A;Reference number: 220061  
 A;Accession: T25639  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-486 <MLI>  
 A;Cross-references: UNIPARC:UPI00001798B5; EMBL:U88314; PIDN:AA842358.1; GSPDB:GN00019;  
 A;Experimental source: strain Bristol N2; clone C46H11  
 A;Genetics:  
 A;Gene: C46H11.4  
 A;Map position: 1  
 A;Introns: 15/3; 190/1; 359/3

T42444 1D-myoinositol-trisphosphate 3-kinase (EC 2.7.1.127) 1 - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: T42444

R;Clandinin, T.R.; Demodena, J.A.; Sternberg, P.W.

Cell 92, 523-533, 1998

A;Title: Inositol triphosphate mediates a RAS-independent response to LBT-23 receptor t

A;Reference number: Z22166; MUID:98150857; PMID:9491893

A;Accession: T42444

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-494 &lt;CL&gt;

A;Cross-references: UNIPROT:045049; UNIPARC:UPI0000076340; EMBL:AF045611; NID:92898157;

C;Genetics: A;Note: LFE-2

C;Keywords: phosphotransferase

Query Match 44.3%; Score 321; DB 2; Length 494;

Best Local Similarity 48.6%; Pred. No. 1.2e-22; Mat ches 67; Conservative 21; Mismatches 48; Indels 2; Gaps 2;

QY 1 AVTKPRYMPQRETMSSTGKTFTRIGIKKADGTCTNFKKTQALEQVTKVLQEDTVGDHV 60

Db 319 AITKLYRQMPFRERSSSTAQJQFRTEAKQKLEGALEKNNFKVVRTVEDVTTFFMDPGTQRS 378

QY 61 -ILQKYVACELLEALETSPPFKTHEVGSSLFLVHDITGLAKWMMIDPGKTVLPHQ 119

Db 379 RVRQQLIERLKLMSMKAIEHSFFNSHEVVGSSILVFD-TEKVSCWMIDPAKSSPVPNGR 437

QY 120 TLSHRLPWAEGNRDGYL 137

Db 438 TLNHTTTWIPGNNEDGYL 455

RESULT 10 (S)

T50224<sup>4</sup> probable arginine metabolism transcription control protein [imported] - fission yeast

C;Species: Schizosaccharomyces pombe

C;Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004

C;Accession: T50224

R;Zimmermann, W.; Wambutt, R.; Mcougall, R.C.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, December 1999

A;Reference number: Z25047

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-268 &lt;ZIM&gt;

A;Cross-references: UNIPROT:09814; UNIPARC:UPI000006AE2B; EMBL:AL135751; PIDN:CAB63791.

A;Experimental source: strain 972n(-); cosmid c607

C;Genetics:

A;Gene: SPDB-SPAC607.04

A;Map position: 1

RESULT 12 (S)

T27707 hypothetical protein ZKL193.3 - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T27707

R;Geisel, C.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of *C. elegans* cosmid ZKL193.

A;Reference number: Z20409

A;Accession: T27707

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-476 &lt;GEI&gt;

A;Cross-references: UNIPROT:Q23410; UNIPARC:UPI00000753E9; EMBL:U41553; PIDN:AAA83292.1;

C;Genetics:

A;Gene: CESP;ZKL193.3

A;Map position: 222/3; 132/1; 182/3; 308/1; 358/3; 403/1

Query Match 12.4%; Score 90; DB 2; Length 268; Best Local Similarity 29.2%; Pred. No. 0.48; Mat ches 40; Conservative 14; Mismatches 43; Indels 40; Gaps 6;

QY 15 SSTS TLGFRIEGIKKADGTCTNFK-----KIQALEQTVKLEDFVGDGHVILQKVA 67

Db 125 STTGSIGFRITGILSWDRNTNTYIKRSTAWKGKTLTSDVTEGLNDP-----FVS 174

QY 68 C-----LLEELREALEISPFKTHEVGSSLFLVHDITGLAKWV-----MI 107

Db 175 OSLSQKARLVESPFLNLKLFLFVLDLSESYIELKSSSLFLVFDYSSNAPTHCESNVVLKLI 234

QY 108 DFGK---TVALPDHQTL 121

Db 235 DLAHSRWTKNTIDHNTL 251

hypothetical protein F45C12.5 - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T32105

R;Johnson, D.; Kramer, J.; Kepler, D.

submitted to the EMBL Data Library, July 1997

A;Description: The sequence of *C. elegans* cosmid F45C12.

A;Reference number: Z22123

A;Accession: T32105

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-555 &lt;JOH&gt;

A;Cross-references: UNIPROT:016745; UNIPARC:UPI0000082C77; EMBL:AF016684; PIDN:AA66215.1

A;Experimental source: strain Bristol N2; clone F45C12

C;Genetics:

A;Gene: CESP;F45C12.5

A;Map position: 2

A;Introns: 26/2; 307/3; 375/3; 465/3

Query Match 10.8%; Score 78; DB 2; Length 555; Best Local Similarity 23.2%; Pred. No. 15; Mat ches 35; Conservative 25; Mismatches 51; Indels 40; Gaps 8;

QY 4 KPRYQWRTMSSTGKTFTRIGIKKANG-----TCTTNPKK-----TQALBQVTKLED 53

Db 175 KPNYQQ---IIVRNLDKFTVENSNDGAGQNLNLASASFIKLTETLSSNQINFLKH 230

QY 54 FVGDGHVILQKVALESLR-----EALESPPFTTHEVGSSLFLVHDHT----- 99

Db 231 WIAGSNEMILRGFM--LEQLEAYNQVSINGLDQPSVREHGHYKENNLYLPRQKENDT 288

QY 100 ---GLAKV--WMLDPGKTVLAPDQHQTSHRL 125

Db 289 RNDGMRATYWALGWQR----HSSLSQRL 314

RESULT 11

T32105

RESULT 13

E70320 polyribonucleotide nucleotidyltransferase - *Aquifex aeolicus*  
 C;Species: *Aquifex aeolicus*  
 C;Date: 05-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
 C;Accession: E70320  
 R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; On  
 V;Nature 392, 353-358, 1998  
 A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.  
 A;Reference number: A70300; MVID:919666; PMID:933730  
 A;Accession: E70320  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-775 <AQP>  
 A;Cross-references: UNIPROT:066593; UNIPARC:UPI00000562CC; GB:AE000679; NID:g2982936; PI  
 A;Experimental source: strain VF5  
 C;Genetics:  
 A;Gene: pspa  
 C;Superfamily: polyribonucleotide nucleotidyltransferase

Query Match 10.7%; Score 77.5; DB 2; Length 775;  
 Best Local Similarity 26.9%; Pred. No. 26;  
 Matches 35; Conservative 23; Mismatches 43; Indels 29; Gaps 7;  
 A;Status: preliminary

Qy 4 KPYMQWREMTNSSTG---FRIEGKIKAGCTCWNPKKQALEQVTK---VLEDIV 55  
 Db 473 KDRYVILSDINGDDEHGDMPKVAGPK---DGI---TSVQMDIKVKGKIKTEMLDALKQR 528

Qy 56 DGDGHVILQKVYVACELLERLREALBISPPKTHWV-----GSSILFVHDHTGL 101  
 Db 529 EGRVLYLEKMKTEAIPPEPKR-EPHPYTPKVSVWDVPEEKAPLILPGGSTVKKIVDETGV 586

Qy 102 AKVWMDDFGK 111  
 Db 587 -KVVWGEQGK 595

RESULT 14  
 AI2002 hypothetical protein alr1575 [imported] - *Nostoc* sp. (strain PCC 7120)  
 C;Species: *Nostoc* sp. PCC 7120  
 A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
 C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C;Accession: AI2002  
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchishi, S.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; DNA Res. 8, 205-213, 2001  
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. AI2002  
 A;Reference number: ABI807; MVID:21593285; PMID:11759840  
 A;Accession: AI2002  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1047 <KUR>  
 A;Cross-references: UNIPROT:Q8YWNO; UNIPARC:UPI00000CE131; GB:BA000019; PIDN:BA877941.1;  
 C;Genetics:  
 A;Gene: alr1575

Query Match 10.5%; Score 76; DB 2; Length 1047;  
 Best Local Similarity 25.2%; Pred. No. 50;  
 Matches 32; Conservative 17; Mismatches 44; Indels 34; Gaps 7;

Qy 36 TNPKKTT---QALQVTKVLEDFFVGDGHVILQKVYVACELLERLREALBISPPKTK---HEVVG 90  
 Db 477 TNFEGDPIYRCLESANMFL---FIISKSLSSPPY-CTTEVYFAMLNKRIKVLYREIKGA 532

Qy 91 SILFVHDHTSIAKVNMDFG-----KIVVALDHPQTLSH----RLPWAEG 130  
 Db 533 TL----HPGLAKVWVIDFSQHNTDFLTKGFBLLTRLDSDEPYVRSHTRIFLKARDWEH 587

Qy 131 NREDEGYL 137  
 Db 588 IRDDSPFL 594

RESULT 15  
 R86391 hypothetical protein TIK7.13 [imported] - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2004  
 C;Accession: R86391  
 R;Theologis, A.; Achter, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.; Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Maiti, R.; Marzali, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A;Reference number: A86141; MVID:21016719; PMID:1130712

A;Accession: R86391  
 A;Molecule type: DNA  
 A;Residues: 1-302 <STO>  
 A;Cross-references: UNIPROT:Q9FZD5; UNIPARC:UPI0000088E7F; GB:AE005172; NID:9979750; PI  
 C;Genetics:  
 A;Map Position: 1  
 C;Superfamily: hypothetical protein containing F-box domain

Query Match 10.3%; Score 75; DB 2; Length 302;  
 Best Local Similarity 30.3%; Pred. No. 15;  
 Matches 27; Conservative 11; Mismatches 31; Indels 20; Gaps 5;

Qy 50 VLEDIVDGVILQKVYVACELLERLREALBISPPKTKHVGSSILVHDHGLAKW-MID 108  
 Db 169 VVKSFRGQYDPVSDQKRVSCMWERRHLRDP-SSERHQV-----TLEKCPWKMD 218

Qy 109 FGKTVALLDPOHQLSLRHPWAEGRNEDGYL 137  
 Db 219 ---CTNSIPDR-----PWSNGVCIDGFV 238

Search completed: May 21, 2006, 04:26:09  
 Job time : 40 secs

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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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OP9475; HUMAN	PRELIMINARY; PRT; 604 AA.
ID	TISSUE=Placenta;
AC	RP NUCLEOTIDE SEQUENCE;
RA	RC TISSUE=Placenta;
RA	RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	RA STRausberg R.L., Fengold E.A., Grouse L.H., Derge J.G.,
RA	RA 01-NOV-1999, integrated into UniProtKB/TREMBL.
RA	RA 01-NOV-1999, sequence version 1.
DT	DT DT 2006, entry version 15.
DE	DE Inositol 1,4,5-trisphosphate 3-kinase isoenzyme (EC 2.7.1.127)
DE	DE (Fragment).
DE	DE Homo sapiens (Human).
DE	DE <i>Yukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens (Human); Mammalia; Eutheria; Euarchontoglires; Primates; Cetartiodactyla; Hominoidea; Hominidae; Neboi-TaxID=9606;</i>
RN	RN [1] NUCLEOTIDE SEQUENCE.
RP	RP TISSUE=Thyroid gland;
RC	RC Takazawa K., Go M., Togashi S., Endo T., Erneux C., Onaya T.,
RA	RA Submitted (SBP-1994) to the EMBL/GenBank/DBJ databases.
RA	RA Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>
RA	RA distributed under the Creative Commons Attribution-NonDerivs License
RA	RA EMBL; D38169; BAA202524; 1; ; mRNA.
RA	RA Ensemble; ENSG0000006544; Homo sapiens.
RA	RA GO; GO:0008440; Pinositol triphosphate 3-kinase activity; IEA.
RA	RA GO; GO:0016301; P:kinase activity; IEA.
RA	RA DR InterPro; IPR05522; IPK.
RA	RA DR Pfam; PF03770; IPK; 1.
KW	KW Kinase; Transferase.
FT	FT NONTER 1
SQ	SQ SEQUENCE 604 AA; 672336 MW; 52AC5AB5FB3F0176 CRC64;
Query Match	100.0%; Score 725; DB 2; Length 604;
Best Local Similarity	100.0%; Pred. No. 5.4e-60;
Matches	137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	Qy 1 AVTKPRIMQWRETMSTSITLGRIGRIGIKKADGTCTNFKKTQALQTVKLEDFVGDHV 60
Db	Db 452 AVTKPRIMQWRETMSTSITLGRIGRIGIKKADGTCTNFKKTQALQTVKLEDFVGDHV 511
Qy	Qy 61 ILQKVKVACELREALEISPFKTKTHEVVGSSLFLVHDHTGLAKVWMDFGKTVLALPDHQ 120
Db	Db 512 ILQKVKVACELREALEISPFKTKTHEVVGSSLFLVHDHTGLAKVWMDFGKTVLALPDHQ 571
Qy	Qy 121 LSHRLPWAEGNRDGYL 137
Db	Db 572 LSHRLPWAEGNRDGYL 588
RESULT 3	RESULT 3
Q6DU7_HUMAN	Q6DU7_HUMAN PRELIMINARY; PRT; 683 AA.
AC	AC Q6DU7; 01-DEC-2001, integrated into UniProtKB/TREMBL.
DT	DT 01-DEC-2001, sequence version 1.
DT	DT 07-FEB-2006, entry version 19.
DE	DE Inositol 1,4,5-trisphosphate 3-kinase C.
GN	GN Name=ITPKC;
OS	OS Homo sapiens (Human).
OC	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC	OC Homo;
OC	OC NCBI_TaxID=9606;
RN	RN [1] NUCLEOTIDE SEQUENCE.
RP	RP TISSUE=Thyroid;
RC	RC TISSUE=Thyroid;
RC	RC MEDLINE=0539319; PubMed=11085927; DOI=10.1032/024-6021:3520343;
RA	RA Dewar V., Puillon V., Moreau C., Shears S., Takazawa K., Erneux C.,
RA	RA "Cloning and expression of a cDNA encoding human inositol 1,4,5-trisphosphate 3-kinase C";
RT	RT Biochem. J. 332:343-351 (2000).
RN	RN [2]
RESULT 4	RESULT 4
Q80ZG2_HUMAN	Q80ZG2_HUMAN PRELIMINARY; PRT; 678 AA.
ID	ID Q80ZG2_RAT PRELIMINARY; PRT; 678 AA.
AC	AC Q80ZG2; 01-JUN-2003, integrated into UniProtKB/TREMBL.
DT	DT 01-JUN-2003, sequence version 1.
DT	DT 07-FEB-2006, entry version 11.
DE	DE Inositol 1,4,5-trisphosphate 3-kinase C.
GN	GN Name=IP3Kc; Synonyms=IP3Kc, ip3k-c;
OS	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

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OM protein - protein search, using SW model

Run on: May 21, 2006, 04:17:09 ; Search time 296 Seconds  
(without alignments)  
(428.132 Million cell updates/sec)

Title: US-10-781-581-226

Perfect score: 725

Sequence: 1 AVTKPQRMQRETMSSSTL.....HQLLHRLPWAEGNREDGYL 137

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext: 0.5

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 7.2:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	725	100.0	137	2 Q9UE25_HUMAN
2	725	100.0	604	2 Q9Y475_HUMAN
3	725	100.0	683	2 Q96DUT_HUMAN
4	660	91.0	678	2 Q802G2_RAT
5	658	90.8	678	2 Q3U384_MOUSE
6	658	90.8	678	2 Q7TS72_MOUSE
7	524	72.3	300	2 Q4SPLO_TETRAODON
8	517	71.3	395	2 Q5RGF8_BRADYMYO
9	514	70.9	452	2 Q9YH85_CHICK
10	513	70.8	400	2 Q5XK93_XENIA
11	513	70.8	516	2 Q2TAE4_XENIA
12	507	69.9	325	2 Q4SC34_TETRAODON
13	505	69.8	425	1 Q4RM63_TETRAODON
14	506	69.8	459	1 Q93KA_MOUSE
15	506	69.8	459	1 IP3KA_RAT
16	504	69.5	461	1 IP3KA_HUMAN
17	496.5	68.5	2 Q8JFUG_BRADY	
18	494.5	68.2	195	2 Q8JFSE_BRADY
19	493	68.0	472	2 Q2T0B2_HUMAN
20	493	68.0	946	1 IP3KA_HUMAN
21	487	67.2	934	1 IP3KB_RAT
22	482	61.0	310	2 Q4S8S8_TETRAODON
23	434	59.9	282	2 Q73595_CHICK
24	410.5	56.6	377	2 Q5TX95_ANOOGA
25	410.5	56.6	398	2 Q7PK9_ANOOGA
26	403.5	55.7	459	2 Q8X8B_DROME
27	403.5	55.7	669	2 Q9YV85_DROME
28	387	53.4	463	2 Q963D4_APIME
29	387	53.4	548	2 Q963D3_APIME
30	387	53.4	782	2 Q963D5_APIME
31	393	53.4	393	2 Q61HC5_CAEEL

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30	387	53.4	782	2 Q963D5_APIME
31	393	53.4	393	2 Q61HC5_CAEEL

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2	725	100.0	604	2 Q9Y475_HUMAN

OC Muroidea; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
 RA Mayz G.W., Bertsch U., Fanick W., Stockebrand M.C., Schmale H.,  
 RA Nalejkowska M.M., Bertsch U., Fanick W., Stockebrand M.C., Schmale H.,  
 RA "Rat inositol 1,4,5-trisphosphate 3-kinase C is enzymatically  
 RT specialized for basal cellular inositol triphosphate phosphorylation  
 RT and shuttles actively between nucleus and cytoplasm.",  
 J. Biol. Chem. 278:19765-19776 (2003).  
 RL [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NODstar; TISSUE=Circumvallate taste papilla;  
 RA Bertsch U., Schmale H., Deschermeier C., Christiansen H., Fanick W.,  
 RA Mayz G.W., Bertsch U., Schmale H., Deschermeier C., Christiansen H., Fanick W.,  
 RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
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 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonDerivs License  
 DR EMBL; AVI160770; AA020335.1; -; mRNA.  
 DR EMBL; AU440783; CAD29464.1; -; mRNA.  
 DR SMR; Q802G2; 420-678.  
 DR Ensembl; ENSG0000013945; Rattus norvegicus.  
 DR RGD; 631336; Itpk.  
 DR GO; GO:00116301; Protein kinase activity; IDA.  
 DR InterPro; IPR005522; IPK.  
 DR Pfam; PF03770; IPK; 1.  
 KW Kinase.  
 SQ SEQUENCE 678 AA; 74463 MW; 5EDEA14255DACD2B CRC64;  
 Query Match 91.0%; Score 660; DB 2; Length 678;  
 Best Local Similarity 92.0%; Pid: No. 9.2e-54;  
 Matthes 126; Conservativity 5; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 AVTKPRYMQWRTMSTSTGPRTEGIKKADGTCTNPKKTQALEQVTKLVEDVGDHV 60  
 Db 526 AVTKPRYMQWRTMSTSTGPRTEGIKKADGTCTNPKKTQALEQVTKLVEDVGDV 585  
 Qy 61 IOKVYACLEBLREALIEIPPFKTHEVVEVSSLLFVHDHGLAKYWMIDRGKTVALPDHQT 120  
 Db 586 IOKVYACLEBLREALIEIPPFKTHEVVEVSSLLFVHDHGLAKYWMIDRGKTVALPDHOM 645  
 Qy 121 LSHRLPWAGRNREDGYL 137  
 Db 646 LSHRLPWAGRNREDGYL 662  
 RESULT 5  
 Q0384 MOUSE PRELIMINARY; PRT; 678 AA.  
 ID Q3U384\_MOUSE PRELIMINARY; PRT; 678 AA.  
 AC Q3U384;  
 DT 11-OCT-2005, integrated into UniProtKB/TREMBL.  
 DT 01-FBB-2006, entry version 5.  
 DE CD16+ve dendritic cells cDNA. RIKEN full-length enriched  
 DE library clone:RG3011023 product:inositol 1,4,5-trisphosphate 3-  
 DE kinase C, full insert sequence.  
 GN Name=Itpk1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Euarchoptoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RX MEDLINE=22354683; PubMed=14246681; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nishida I., Osato N., Saito R., Suzuki H., Yamamoto T., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa T., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Rame D.A., Quackenbush J.,  
 RA Schriml L.M., Kamapin A., Matsuda H., Batyalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Choctia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gasteriand S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Meglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Megashima T., Numata K., Okido T., Pavan W.J., Perera G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takehara Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wyrshaw-Boris A., Yangagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Nakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kogawa I.,  
RA Miyazaki A., Sakai K., Sakaai D., Shibata K., Shingawa K.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL *Nature* 420:563-573 (2002).  
RN [15]

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NOD;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi K.Y., Konno H., Adachi J., Fukuda S.,  
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kakuwa T., Saito R.,  
RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaatland T., Gissi C., Gion B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume N.H., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoen C., Sева T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Witz C., Whittaker C., Wilming L.,  
RA Wyrshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J.H., Kohsukii S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL *Nature* 409:685-690 (2001).  
RP [6]

RC NUCLEOTIDE SEQUENCE.  
RX MEDLINE=2149374; PubMed=11042159; DOI=10.1101/gr.45100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RT "Normalizierung und Subtraktion von cap-trapper-selektierten cDNAs zu  
RT der Erstellung von vollständigen cDNA-Librarären für die schnelle Entdeckung neuer Gene.";  
RL Genome Res. 10:1617-1630 (2000).  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NOD;  
RX MEDLINE=20510913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Kojino H., Akiyama J., Nishi K., Kitsuina T., Tachiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto S., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wakahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771 (2000).  
RN [16]

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NOD;  
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,  
RA Hori F., Iida J., Immamura K., Imotani K., Itoh M., Kanagawa S.,  
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sakaai D.,  
RA Shibata K., Shiraki T., Tagami M., Tadami Y., Waki K., Watahiki A.,  
RA Muramatsu M., Hayashizaki Y.,  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

DR MGI; MGI:2442554; IPD-KC.  
DR GO:000440; F:inositol triphosphate 3-kinase activity; IDA.  
DR InterPro; IPR005522; IPK.  
DR Pfam; PF03770; IFF; 1.  
KW Kinase.

SQ SEQUENCE 678 AA; 74492 MW; 61DCB3F3CC6B807 CRC64;

Q9 Query Match 90.8%; Score 658; DB 2; Length 678;  
Q9 Best Local Similarity 91.2%; Pred. No. 1. 4e-53;  
Q9 Matches 125; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
Q9 Result 6

DB 526 AITKPRKPYQWQRELTLSSTLGRFRIEGKKGAGTCNTNFKKTOALSYTKVLEDFVGDGHV 60

Q9 61 ILQKVKACLEERALELISPFFKTHEWVGSSLVEVDHTGLAKVWNIDFGKTVALDPQT 120

DB 586 LIRKVKVLEDRLETRLENSPFKTHEVGGSSLFVDTGAKVWNIDFGKTVALDPQM 645

Q9 121 LSHRLPWAEGNEDGYL 137

DB 646 LSHRLPWTEGNEDGYL 662

DR 07-FEB-2005, entry version 13.  
DE Inositol 1,4,5-trisphosphate 3-kinase C.  
GN Name=IPKc;  
OS *Mus musculus* (Mouse);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuromorphi;  
OC Muridae; Muridae; Murinae; Mus.  
OK NEBI\_TaxID=10090;  
RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE-Limb;  
RX MEDLINE=22388257; PubMed=12477332; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F.,  
RA Dbatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loqueilano N.A., Peters C.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Falney J., Heaton B., Kettman M., Madden A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young E.D., Shvchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.E.,  
RA Scherch A., Schain J.E., Jones S.J.M., Marr M.A.,  
RA "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE-Limb;  
RA Strausberg R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

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CC EMBL; BC053450; AAH53450.1; -; mRNA.  
DR SMR; Q7TS72; 420-678.





OS *Xenopus laevis* (African clawed frog).  
 OC *Bukaryota*; *Metazoa*; *Chordata*; *Craniata*; *Vertebrata*; *Euteleostomi*; DE *Amphibia*; *Batrachia*; *Anura*; *Mesobatrachia*; *Pipoidea*; *Pipidae*; OC *Xenopidae*; *Xenopus*; *Xenopus*.  
 OX NCBI\_TAXID=8355;  
 RN [1] NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Spleen;  
 RX MEDLINE=223341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.-L., Strausberg R. L., Wagner L., Pontius J., Clifton S. W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus* initiative";  
 RL Dev. Dyn. 225:384-391 (2002).  
 RN [2] NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R. L., Fengold E. A., Grouse L. H., Derge J. G., Schneen C. M., Sheppard G. D.,  
 RA Klausner R. D., Collins F. S., Wagner L., Schaefer C. F., Bhat N. K.,  
 RA Altschul S. F., Zeeberg B., Butow K. H., Schaefer C., Ozouf-Costaz C., Bernat A.,  
 RA Hopkins R. F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A. A., Rubin G. M., Hong L.,  
 RA Stapleton M., Soares M. B., Bonaldo M. F., Casavant T. L., Schatz T. E.,  
 RA Brownstein M. J., Usdin T. B., Toshiriki S., Carninci P., Prange C.,  
 RA Hahn S. S., Loqueland N. A., Peters G. J., Abramson R. D., Mulahay S. J.,  
 RA Bosak S. A., McEwan P. J., McKernan K. J., Malek J. A., Gunaratne P. H.,  
 RA Richards S., Worley K. C., Hale S., Garcia A. M., Gay L. J., Hulyk S. W.,  
 RA Villalon D. K., Muzny D. M., Sodergren E. J., Lu X., Gibbs R. A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G.,  
 RA Blakeley R. W., Toucman J. W., Green E. D., Dickson M. C.,  
 RA Rodriguez A. C., Grinwood J., Schmutz J., Myers R. M.,  
 RA Butterfield Y. S.-N., Krzywinski M. I., Skalska U., Smialus D. E.,  
 RA Schenck A., Schein J. E., Jones S. J. M., Marra M. A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [3] NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RA Klein S., Gerhard D. S.,  
 RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonDerivs License  
 CC EMBL: BC110967; AA110968-1; -; mRNA.  
 DR Hypothetical protein.  
 KW SEQUENCE 516 AA; 58271 MW; 2693D817D8AD957A CRC64;  
 SQ

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 Matches 97; Conservative 17; Mismatches 23; Indels 0; Gaps 0;  
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 SEQ 325 AA; 37051 MW; DABAD751ABE35AC5 CRC64;

Query Match 69.9%; Score 507; DB 2; Length 325;  
 Best Local Similarity 69.1%; Pred. No. 1.4e-39;  
 Matches 94; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
 FPT NON\_TER 325 325  
 SEQ 325 AA; 37051 MW; DABAD751ABE35AC5 CRC64;

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 Best Local Similarity 69.1%; Pred. No. 1.4e-39;  
 Matches 94; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
 FPT NON\_TER 325 325  
 SEQ 325 AA; 37051 MW; DABAD751ABE35AC5 CRC64;

Qy 1 AVTKPRYMQWRTMSSTSITGFRIGKIKADGTCTNFKKTOQALEQVTKYLEDYFDVGDHV 60  
 Qy 364 AILKPRYMQWRTMSSTSITGFRIGKIKADGTCTNFKKTOQALEQVTKYLEDYFDVGDHV 60  
 Db 177 VTKPRYMQWRTMSSTSITGFRIGKIKADGTCTNFKKTOQALEQVTKYLEDYFDVGDHV 60  
 Qy 61 ILQKVYACELREALELISPFPKTHEVVGSSLFVHDHTGAKVNMIDRGKTVALPDHOT 120  
 Db 424 1LRKVYVRLKSLTALEKSEFFQSHEVVGSSLFVHDSSQAKVNMIDFGKTVRLPCTQI 483  
 Qy 121 ILSRHPWAGNRGEGYL 137  
 Db 484 IAHRPWAGNRGEGYL 500

RESULT 13  
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 ID Q4RM63\_TETNG PRELIMINARY; PRT; 425 AA.  
 AC Q4RM63;  
 DT 19-JUL-2005, integrated into UniProtKB/Trembl.  
 DT 19-JUL-2005, sequence version 1.  
 DT 07-FEB-2005, entry version 4.  
 DE Chromosome 10 SCARF5019 whole genome shotgun sequence. (Fragment).  
 GN ORFNames=GSTENG00032195001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC *Bukaryota*; *Metazoa*; *Chordata*; *Craniata*; *Vertebrata*; *Euteleostomi*; DE *Actinopterygii*; *Neopterygii*; *Teleostei*; *Euteleostei*; *Neoteleostei*; OC *Acanthomorpha*; *Acanthopercyigii*; *Percomorpha*; *Tetraodontiformes*; OC *Tetradontida*; *Tetraodontidae*; *Tetraodon*.  
 RN [1] NCBI\_TAXID=9883;

RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15196914; DOI=10.1038/nature03025;  
 RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jabin C., Castelloi V., Vacherie B.,  
 RA Blimont C., Skalli Z., Cattolico L., Poulin J., De Bernardini V.,  
 RA Cruaud C., Duprat S., Brottier P., Courteau J.-P., Gouzy J.,  
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Voiff J.-N., Guigo R., Zody M.C., Melsirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D. D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Querier P., Saurin W., Scarpelli C.,  
 RA Wincher P., Lander E.S., Weissenbach J., Roest Crollius H.,  
 RT "Genome duplication in the teleost fish *Tetraodon nigroviridis* reveals  
 the early vertebrate proto-karyotype";  
 RL Nature 431:946-957 (2004).  
 RN [2] NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC - CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC NUCLEOTIDE SEQUENCE.  
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 CC EMBL: CAAB01014660; CAG01798.1; -; Genomic\_DNA.  
 DR GO; GO:0008440; F:inositol triphosphate 3-kinase activity; IEA.  
 DR GO; GO:0008440; F:inositol triphosphate 3-kinase activity; IEA.  
 FPT NON\_TER 1 1  
 SEQ 325 AA; 37051 MW; DABAD751ABE35AC5 CRC64;

Query Match 69.9%; Score 507; DB 2; Length 325;  
 Best Local Similarity 69.1%; Pred. No. 1.4e-39;  
 Matches 94; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
 FPT NON\_TER 325 325  
 SEQ 325 AA; 37051 MW; DABAD751ABE35AC5 CRC64;

Qy 2 VTKPRYMQWRTMSSTSITGFRIGKIKADGTCTNFKKTOQALEQVTKYLEDYFDVGDHV 61  
 Db 237 LKCYLSRLERDTLTSPPFKAHENVGSSLFVHDSTGAKVNMIDRGKTVALPDHOT 121  
 Qy 122 SHRLPWAEGNRGEGYL 137  
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 AC Q4SC34;  
 DT 19-JUL-2005, integrated into UniProtKB/Trembl.  
 DT 07-FEB-2005, entry version 4.  
 DE Chromosome 10 SCARF5019 whole genome shotgun sequence. (Fragment).  
 GN ORFNames=GSTENG00032195001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC *Bukaryota*; *Metazoa*; *Chordata*; *Craniata*; *Vertebrata*; *Euteleostomi*; DE *Actinopterygii*; *Neopterygii*; *Teleostei*; *Euteleostei*; *Neoteleostei*; OC *Acanthomorpha*; *Acanthopercyigii*; *Percomorpha*; *Tetraodontiformes*; OC *Tetradontida*; *Tetraodontidae*; *Tetraodon*.  
 RN [1] NCBI\_TAXID=9883;

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 ID Q4SC34\_TETNG PRELIMINARY; PRT; 325 AA.  
 AC Q4SC34;  
 DT 19-JUL-2005, integrated into UniProtKB/Trembl.



RESULT 15	IP3K, RAT	STANDARD:	PRT;	459 AA.
ID	IP3K, RAT			
AC	P17105;			
DT	01-AUG-1990, integrated into UniProtKB/Swiss-Prot.			
DT	01-NOV-1991, sequence version 3.			
DT	07-FEB-2006, entry version 42.			
DE	Inositol-trisphosphate 3-kinase A (EC 2.7.1.127) (Inositol 1,4,5-trisphosphate 3-kinase A) (IP3K A) (IP3 3-kinase A).			
GN	Name=Ip3ka;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Rattus.			
OC	NCBI TaxID=10116;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [mRNA].			
RX	Medline=91090700; PubMed=2176078;			
RA	Takazawa K., Vandekerckhove J., Dumont J.E., Erneux C.;			
RT	"Cloning and expression in <i>Escherichia coli</i> of a rat brain cDNA encoding a Ca2+/calmodulin-sensitive inositol 1,4,5-trisphosphate 3-kinase.";			
RL	Biocchem. J. 272:107-112(1990).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [mRNA], AND PARTIAL PROTEIN SEQUENCE.			
RC	TISSUE=Brain;			
RT	Medline=9008336; PubMed=2157285;			
RA	Choi K.Y., Kim H.K., Lee S.Y., Moon K.H., Sim S.S., Kim J.W., Chung H.K., Rhee S.G.;			
RT	"Molecular cloning and expression of a complementary DNA for inositol 1,4,5-trisphosphate 3-kinase.";			
RL	Science 248:64-66(1990).			
RN	[3]			
RP	PROTEIN SEQUENCE OF 315-326, AND ACTIVE SITE.			
RA	Medline=9534430; PubMed=7666431;			
RT	Commey D., Lecocq R., Vanweyenberg V., Erneux C.;			
RT	"Active site labelling of inositol 1,4,5-trisphosphate 3-kinase by phenylglyoxal.;"			
RL	Biochem. J. 310:109-115 (1995).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 185-459 IN COMPLEX WITH ADP.			
RA	Miller G.J., Hurley J.H.;			
RT	"Crystalline structure of the catalytic core of inositol 1,4,5-trisphosphate 3-kinase.";			
RL	Mol. Cell 15:703-711(2004).			
CC	- - CATALYTIC ACTIVITY: ATP + 1D-myoinositol 1,4,5-trisphosphate = ADP + 1D-myoinositol 1,3,4,5-tetrakisphosphate.			
CC	- - ENZYME REGULATION: IP3K is activated by calmodulin.			
CC	- - SIMILARITY: Belongs to the inositol phosphokinase (IPK) family.			
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>			
CC	Distributed under the Creative Commons Attribution-NonDerive License			
CC	-----			
DR	EMBL: X56917; CAA40248.1; -; mRNA.			
DR	EMBL: M29707; AAA41457.1; ALT_INIT; mRNA.			
DR	PIR: S13064; S13064.			
DR	PDB; 1T2D; X-ray; A/B=185-459.			
DR	Ensembl; ENSRNOG000000005284; Rattus norvegicus.			
DR	IntAct; IPRO0522; IPK.			
DR	RGD; 619950; IPK. 1.			
DR	3D-structure; Adp-binding; Calmodulin-binding; Direct protein sequencing; Kinase; Nucleotide-binding; Transferase.			
DR	GO; GO:0005440; F:inositol triphosphate 3-kinase activity; IDA. . . . IDA.			
DR	InterPro; IPR00522; IPK.			
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DR	GO; GO:0004685; F:calcium- and calmodulin-dependent protein k. . . . IDA.			
DR	IntAct; IPRO0522; IPK.			
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DR	3D-structure; Adp-binding; Calmodulin-binding; Direct protein sequencing; Kinase; Nucleotide-binding; Transferase.			
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FT	Inositol-trisphosphate 3-kinase A.			
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QY	121	LSHLRPLWAEGRGEGDGL 137		
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Mon May 22 09:43:34 2006

us-10-781-581-226.rup

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Search completed: May 21, 2006, 04:25:26  
Job time : 299 secs

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GenCore version 5.1.8

protein - protein search, using sw model

May 21, 2006, 04:25:44 ; Search time 50 Seconds  
(without alignments)

239.834 Million cell updates/sec

fect score: 725

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oring table: BLOSUM62

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searched: 650591 seqs, 87530528 residues

total number of hits satisfying chosen parameters: 650591

maximum DB seq length: 0

maximum DB seq length: 200000000

set-processing: Minimum Match 0 %

Maximum Match 100 %

Listing first 45 summaries

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/8\_COMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/9\_PCTUS\_COMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/10\_COMB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfile11.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	493	68.0	472	2 US-09-949-016-6194
3	493	68.0	504	2 US-09-949-016-8219
4	403.5	55.7	397	2 US-09-270-767-33291
5	403.5	55.7	397	2 US-09-270-767-48508
6	74.5	10.3	390	2 US-09-107-532A-6615
7	72.5	10.0	817	2 US-09-543-681A-4637
8	71	9.8	2141	2 US-09-543-681A-6919
9	70	9.7	274	2 US-10-104-047-3353
10	70	9.7	645	2 US-09-315-127-8
11	70	9.7	645	2 US-09-315-127-9
12	70	9.7	654	2 US-09-315-127-11
13	70	9.7	654	2 US-09-315-127-12
14	69.5	9.6	833	1 US-09-844-086-2
15	69.5	9.6	833	2 US-09-018-211-2
16	69	9.5	260	2 US-09-328-352-6563
17	69	9.5	293	2 US-10-094-749-127-0
18	69	9.5	632	2 US-09-315-127-2
19	69	9.5	632	2 US-09-315-127-3
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RESULTS

Result ID	Score	Query Match Length	DB ID	Description
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ALIGNMENTS

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Sequence 10729, A
Sequence 7730, AP
Sequence 3750, AP
Sequence 3196, AP
Sequence 709, APP
Sequence 275, APP
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli

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RESULT 6  
US-09-107-532A-6615  
; Sequence 6615, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02454  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD/ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107-532A  
; FILING DATE: 30-JUN-1998  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: JULY 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arinello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781) 893-5007  
; TELEFAX: (781) 893-8277  
; INFORMATION FOR SEQ ID NO: 6615:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 390 amino acids  
; TYPE: amino acid  
; TOPeOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1..390  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6615:  
; US-09-107-532A-6615  
Query Match 10.3%; Score 74.5; DB 2; Length 390;  
Best Local Similarity 29.7%; Pred. No. 2.9;  
Matches 33; Conservative 10; Mismatches 31; Indels 37; Gaps 5;  
Qy 37 NPKKIQALEQVTK-----VLEDYDGVIVLQKVKVACELRERALEISPFKTH 85  
Db 190 DPKLSEVLENDTEKVALTEEEQEOAALSLPSFIKTDVYHKYIDMLLILKIGRIS----- 243  
Qy 86 EYVGSSLFLFHDHGLAKYWMIDPKGKTVALPDQIOTSLRHPWAEGRNEDGY 136  
Db 244 ELCG--LTIVAD-----IDFKNEWVILDHOLK-----NKGQGY 274  
RESULT 7  
US-09-43-601A-4637  
; Sequence 4637, Application US/09543681A  
; Patent No. 660709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; SEQ ID NO: 437  
; LENGTH: 817  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
; US-09-543-681A-4637  
Query Match 10.0%; Score 72.5; DB 2; Length 817;  
Best Local Similarity 25.2%; Pred. No. 15;  
Matches 28; Conservative 21; Mismatches 31; Indels 31; Gaps 5;  
Qy 40 KTOALEQVTKLEPFDVGPVHILQKVY-----ACELEL--REALBISPFK 83  
Db 260 KTDALANGVKKVKG---HNLYNKYTIGINGNSQGEVYVSLVEQINDKESITISQND 315  
Qy 84 THEVUGSSLFLVHONTGLAKWMMDFGKVALPDHQTSRHLPAEGNRD 134  
Db 316 TAAFFGISAFAHLSNIGVAFLLANFAKTHA-----TKS-----NQD 355  
RESULT 8  
US-09-949-016-10918  
; Sequence 10918, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENIER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 10918  
; LENGTH: 2141  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-949-016-10918  
Query Match 9.8%; Score 71; DB 2; Length 2141;  
Best Local Similarity 21.6%; Pred. No. 88;  
Matches 35; Conservative 20; Mismatches 53; Indels 54; Gaps 5;  
Qy 8 MQRBT-----MSSTSTGFRIGEKGKADGTCNTNF-----KRTQ 42  
Db 1920 LSNNMSTIQRQETQERPPDVSSYELMMKQGINAEETRSQNSFACALEGELSLLQRQHQ 1979  
Qy 43 ALRQVTKLEPFDVGPVHILQKVACELRERALEISPFKTHEWVGSSLFLVHDHGLA 102  
Db 1980 ASSEIRELQQVMSRKKEMNEKWEARWERLMLLEVQFSRDAV-----A 2025  
Qy 103 KVWMI-----DRGKTVALPDHQTSR-----LPWAB 129  
Db 2026 EAWLIAQPYLASFGEFGHTVDSVEKLTKRHEAFKSTASWE 2067  
RESULT 9  
US-10-104-047-3353  
; Sequence 3353, Application US/10104047  
; Patent No. 694241  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE



OTHER INFORMATION: 8 envelope protein produced by retroviral vector  
; OTHER INFORMATION: of seq. id no. 7  
; US-09-315-127-12

Query Match 9.7%; Score 70; DB 2; Length 654;  
 Best Local Similarity 29.2%; Pred. No. 21; Mismatches 46; Indels 14; Gaps 5;  
 Matches 31; Conservative 15; Mismatches 46; Indels 14; Gaps 5;

Qy 11 RFTMSSTSTL--GFRIGIIRRKADGTCNTNKKTALEQVTKVLE--DFVFDGHVILQK 64  
 Db 458 REPVSITLALLIGLGLRNGGIAAGIGTTTALKTQDPEQHAAIQFDLNEVEKTNLEK 517

Qy 65 YVACLEL---REALRISPKTHEVWGS--SLLFVHDHTGLAK 103  
 Db 518 SITLSLSEVWLNRRGGLDL-LIKEGLCAALKKECCFPYADHTGLVR 562

RESULT 14  
 US-08-844-086-2  
 Sequence 2, Application US/08844086  
 Patent No. 5866390

GENERAL INFORMATION:  
 APPLICANT: Lawlor, Elizabeth  
 TITLE OF INVENTION: No. 5866390el Compounds  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: SmithKline Beecham Corporation  
 STREET: 709 Swedeland Road  
 CITY: King of Prussia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19406-0939

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/844,086  
 FILING DATE: 18-APR-1997  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 960793.4  
 FILING DATE: 18-APR-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gimmi, Edward R  
 REGISTRATION NUMBER: 38,891  
 REFERENCE/DOCKET NUMBER: P31457-4  
 TELEPHONE: 610-270-4478  
 TELEFAX: 610-270-5090

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 610-270-4478  
 TELEX: 610-270-5090

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 833 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-844-086-2

Query Match 9.6%; Score 69.5; DB 2; Length 833;  
 Best Local Similarity 23.7%; Pred. No. 34; Mismatches 40; Indels 47; Gaps 6;  
 Matches 31; Conservative 13; Mismatches 40; Indels 47; Gaps 6;

Qy 37 NPKKIQALEQVTKVLEDFVQG--DAVILQKVYVACLEE-----LREALRISPKF 83  
 Db 366 NVEEAYTEGHLVNSDFLQGINKEDAIKIVACLEEKGGQEKVYTRLDWL----FS 420

Qy 84 THEVWGSISLFLVHDHTGLAKWMDFGKUTVALP-----HOTLSR 124  
 Db 421 RQRWYGPITIH-----W-EDGTSVAVPELPLVLPVTKDIRPSGTGESPLNL 470

Db 366 NVEEAYTEGHLVNSDFLQGINKEDAIKIVACLEEKGGQEKVYTRLDWL----FS 420

Qy 84 THEVWGSISLFLVHDHTGLAKWMDFGKUTVALP-----HOTLSR 124  
 Db 421 RQRWYGPITIH-----W-EDGTSVAVPELPLVLPVTKDIRPSGTGESPLNL 470

Search completed: May 21, 2006, 04:27:04  
 Job time : 51 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 21, 2006, 04:26:24 ; Search time 176 Seconds  
(without alignments)

30.571 Million cell updates/sec  
US-10-781-581-226  
Perfect score: 725  
Sequence: 1 AVTKPRVMQWREMTMSSTL.....HOTLSHRLPWAGNREDDGYL 137

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext: 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /EMC\_Celerra\_SDSD3/ptdata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /EMC\_Celerra\_SDSD3/ptdata/2/pubpaa/US08\_PUBCOMB.pep:\*

3: /EMC\_Celerra\_SDSD3/ptdata/2/pubpaa/US09\_PUBCOMB.pep:\*

4: /EMC\_Celerra\_SDSD3/ptdata/2/pubpaa/US10\_PUBCOMB.pep:\*

5: /EMC\_Celerra\_SDSD3/ptdata/2/pubpaa/US11\_PUBCOMB.pep:\*

6: /EMC\_Celerra\_SDSD3/ptdata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Match Length DB ID Description

1 725 100.0 137 5 US-10-781-581-226 Sequence 226, App

2 725 100.0 660 4 US-10-311-034-26 Sequence 26, App

3 725 100.0 683 4 US-10-092-900A-342 Sequence 342, App

4 493 68.0 798 4 US-10-168-562-5 Sequence 5, Appli

5 493 68.0 798 4 US-10-0979-095-5 Sequence 5, Appli

6 482 66.5 1192 5 US-10-764-330-1 Sequence 1, Appli

7 464 64.0 1339 4 US-10-082-830-282 Sequence 282, App

8 403.5 55.7 382 6 US-11-097-143-1725 Sequence 1725, App

9 382.5 52.8 316 4 US-10-042-894A-5 Sequence 25, Appli

10 145 20.0 71 4 US-10-029-366-29832 Sequence 29832, A

11 81.5 11.2 325 4 US-10-408-1520 Sequence 1520, AP

12 80.5 11.1 349 4 US-10-369-93-175 Sequence 175, AP

13 79.5 11.0 248 6 US-11-096-558A-22990 Sequence 32990, A

14 79.5 11.0 300 6 US-11-096-568A-32989 Sequence 32989, A

15 79 10.9 330 6 US-11-096-568A-32988 Sequence 32988, A

16 79 10.9 422 6 US-11-188-288-12964 Sequence 12964, A

17 78 10.8 279 4 US-10-042-894A-10 Sequence 10, Appli

18 78 10.6 279 4 US-10-424-59-249309 Sequence 249309, A

19 77 10.6 298 5 US-10-506-454-333 Sequence 333, App

20 76 10.5 496 4 US-10-767-701-43815 Sequence 43815, A

21 75.5 10.4 392 4 US-10-437-963-202651 Sequence 202651, A

22 75.5 10.4 977 4 US-10-467-535-1 Sequence 1, Appli

23 75 10.3 317 4 US-10-425-114-51119 Sequence 51119, A

24 75 10.3 455 4 US-10-425-114-42633 Sequence 42633, A

25 74 10.2 335 6 US-11-096-568A-24584 Sequence 24584, A

26 74 10.2 417 4 US-10-437-863-203451 Sequence 203451, A

27 74 10.2 449 6 US-11-096-568A-24583 Sequence 24583, A

RESULT 1  
US-10-781-581-226  
Sequence 226, Application US/10781581  
; Publication No. US20050019746A1  
; GENERAL INFORMATION:  
; APPLICANT: Birx Therapeutics Ltd.  
; APPLICANT: Seery, Liam  
; APPLICANT: Hayes, Ian  
; APPLICANT: Murphy, Finbarr  
; TITLE OF INVENTION: Apoptosis-Related Kinase/GPCRs  
; FILE REFERENCE: 8912/2015  
; CURRENT APPLICATION NUMBER: US/10/781, 581  
; CURRENT FILING DATE: 2004-02-08  
; PRIOR APPLICATION NUMBER: US 10/764, 238  
; PRIOR FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: US 60/457, 533  
; PRIOR FILING DATE: 2003-03-25  
; NUMBER OF SEQ ID NOS: 226  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 226  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-781-581-226  
Query Match 100.0%; Score 725; DB 5; Length 137;  
Best Local Similarity 100.0%; Pred. No. 4.1e-73; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 137; Conservative 0;  
Sequence 137; Conservative 0;  
Sequence 1725, App  
QY 1 AVTKPRVMQWREMTMSSTGPRIGKIKRAGDTCTNFKKTOALEQVTKLEDFRDGHV 60  
1 AVTKPRVMQWREMTMSSTGPRIGKIKRAGDTCTNFKKTOALEQVTKLEDFRDGHV 60  
Db 61 ILQKTYVACLEBLREALIEISPFKTHEVVESSLFLVHDHGLAKYWMIDFGKTVLDPHQ 120  
61 ILQKTYVACLEBLREALIEISPFKTHEVVESSLFLVHDHGLAKYWMIDFGKTVLDPHQ 120  
Db 61 ILQKTYVACLEBLREALIEISPFKTHEVVESSLFLVHDHGLAKYWMIDFGKTVLDPHQ 120  
121 LSHRLPWAGNREDDGYL 137  
121 LSHRLPWAGNREDDGYL 137

RESULT 2  
US-10-311-034-26  
Sequence 26, Application US/10311034  
; Publication No. US20040023242A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.

Sequence 342, Application US/10092900A  
 Publication No. US2004043382A1  
 GENERAL INFORMATION:  
 APPLICANT: Padigari, Muralidara  
 APPLICANT: Spytek, Kimberly A.  
 APPLICANT: Shney, Suresh G.  
 APPLICANT: Taurier Jr., Raymond J.  
 APPLICANT: Pena, Carol E.A.  
 APPLICANT: Li, Li  
 APPLICANT: Zarhusen, Bryan D.  
 APPLICANT: Gusev, Vladimir Y.  
 APPLICANT: Ji, Weizhen  
 APPLICANT: German, Linda  
 APPLICANT: Miller, Charles B.  
 APPLICANT: Kekuda, Rameeh  
 APPLICANT: Paturrajan, Meera  
 APPLICANT: Gangolli, Esha A.M.  
 APPLICANT: Varnet, Corine A.M.  
 APPLICANT: Cho, Xiaojaia Sasha  
 APPLICANT: Tchernev, Velizar T.  
 APPLICANT: Fernandes, Elma R.  
 APPLICANT: Casman, Stacie J.  
 APPLICANT: Malyankar, Uriel M.  
 APPLICANT: Liu, Yi  
 APPLICANT: Anderson, David W.  
 APPLICANT: Spaderna, Steven K.  
 APPLICANT: Catterton, Elina  
 APPLICANT: Leite, Mario W.  
 APPLICANT: Zhong, Haihong  
 APPLICANT: Alsobrook, John P.  
 APPLICANT: Lepley, Denise M.  
 APPLICANT: Rieger, Daniel K.  
 APPLICANT: Burgess, Catherine E.  
 TITLE OF INVENTION: Human Proteins and Nucleic Acids Encoding Same  
 FILE REFERENCE: 21492-290C  
 CURRENT APPLICATION NUMBER: US/10/092,900A  
 CURRENT FILING DATE: 2002-03-07  
 PRIORITY APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;  
 PRIORITY FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0  
 25  
 NUMBER OF SEQ ID NOS: 52  
 SOFTWARE: PERL Program  
 SEQ ID NO: 26  
 LENGTH: 660  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc. feature  
 OTHER INFORMATION: Incyte ID No. US20040023242A1 7480774CD1  
 US-10-311-034-26

Query Match 100.0%; Score 725; DB 4; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-72;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVTKPRYMRQWREMSSTSSTGFRLEGIKADGTCTNFKKTQALEQVTKLVEDFVGDHV 60  
 Db 508 AVTKPRYMRQWREMSSTSSTGFRLEGIKADGTCTNFKKTQALEQVTKLVEDFVGDHV 567  
 Qy 61 ILQKQVACLEELREALISPFKTHRVVGSSLLFVHDHTGAKVWMDFGKTVLDPHQ 120  
 Db 568 ILQKQVACLEELREALISPFKTHRVVGSSLLFVHDHTGAKVWMDFGKTVLDPHQ 627

Query Match 100.0%; Score 725; DB 4; Length 683;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-72;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVTKPRYMRQWREMSSTSSTGFRLEGIKADGTCTNFKKTQALEQVTKLVEDFVGDHV 60  
 Db 531 AVTKPRYMRQWREMSSTSSTGFRLEGIKADGTCTNFKKTQALEQVTKLVEDFVGDHV 590

RESULT 3  
 US-10-092-900A-342

QY 61 IIQKYVACELREALEISPFKTHEVGSSLFVHDHTGLAKVWMIDFGKTVALPDHOT 120 ; APPLICANT: YAO, Monique G.  
Db 591 IIQKYVACELREALEISPFKTHEVGSSLFVHDHTGLAKVWMIDFGKTVALPDHOT 650 ; APPLICANT: LAL, Preetai.  
; APPLICANT: KAHN, Farrah A.  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0002 PCT  
; CURRENT APPLICATION NUMBER: US/10/979,095  
; CURRENT FILING DATE: 2004-11-02  
; PRIORITY APPLICATION NUMBER: US/10/168,582  
; PRIORITY FILING DATE: 2002-06-20  
; PRIORITY APPLICATION NUMBER: 60/172,066; 60/176,107; 60/176,107; 60/177,731  
; NUMBER OF SEQ ID NOS: 24  
; PRIORITY FILING DATE: 1999-12-23; 2000-01-14; 2000-01-21  
; SOFTWARE: PERL Program  
; SEQ ID NO: 5  
; LENGTH: 798  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: misc. feature  
; NAME/KEY: misc. feature  
; OTHER INFORMATION: Incyte ID No: 2902460CD1  
; US-10-979-095-5

Query Match 68.0%; Score 493; DB 4; Length 798;  
Best Local Similarity 67.9%; Pred. No. 58-46; Matches 93; Conservative 14; Mismatches 30; Indels 0; Gaps 0;  
Matches 93; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

QY 1 AVTKPRYMQMRETMSTSSTLGFRIEGIKKAGTCNTNPKKTOALKVLEDFVGDHV 60 ; APPLICANT: YAO, Monique G.  
Db 642 AVTKPRYMQMRETTISSTATLGFRIEGIKKAGTCNTNPKKTOALKVLEDFVGDHV 701 ; APPLICANT: LAL, Preetai.  
; APPLICANT: KAHN, Farrah A.  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0002 PCT  
; CURRENT APPLICATION NUMBER: US/10/168,582  
; CURRENT FILING DATE: 2002-06-20  
; PRIORITY FILING NUMBER: 60/172,066; 60/176,107; 60/176,107; 60/177,731  
; PRIORITY FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PERL Program  
; SEQ ID NO 5  
; LENGTH: 798  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: misc. feature  
; NAME/KEY: misc. feature  
; OTHER INFORMATION: Incyte ID No. US20040058426A1 2902460CD1  
; US-10-168-582-5

RESULT 6 US-10-764-330-1 ; APPLICANT: YAO, Monique G.  
; Sequence 1, Application US/10/764330  
; Publication No. US20040265790A1  
; GENERAL INFORMATION:  
; APPLICANT: Cooke, Michael P.  
; APPLICANT: Sauer, Karsten  
; APPLICANT: Wiltshire, Tim  
; APPLICANT: Tarantino, Lisa  
; APPLICANT: Fletcher, Colin  
; APPLICANT: Wen, Ben  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING T LYMPHOCYTES  
; FILE REFERENCE: PI097US10  
; CURRENT APPLICATION NUMBER: US/10/764,330  
; CURRENT FILING DATE: 2004-01-23  
; PRIORITY APPLICATION NUMBER: US 60/442,792  
; PRIORITY FILING DATE: 2003-01-25  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 1  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-10-764-330-1

Query Match 66.5%; Score 482; DB 5; Length 1192;  
Best Local Similarity 67.2%; Pred. No. 1.58-44; Matches 92; Conservative 14; Mismatches 31; Indels 0; Gaps 0;  
Matches 92; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

QY 1 AVTKPRYMQMRETMSTSSTLGFRIEGIKKAGTCNTNPKKTOALKVLEDFVGDHV 60 ; APPLICANT: YAO, Monique G.  
Db 869 AVTKPRYMQMRETTISSTATLGFRIEGIKKAGTCNTNPKKTOALKVLEDFVGDHV 928 ; APPLICANT: LAL, Preetai.  
; APPLICANT: KAHN, Farrah A.  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0002 PCT  
; CURRENT APPLICATION NUMBER: US/10/979,095  
; CURRENT FILING DATE: 2004-11-02  
; PRIORITY APPLICATION NUMBER: US/10/168,582  
; PRIORITY FILING DATE: 2002-06-20  
; PRIORITY APPLICATION NUMBER: 60/172,066; 60/176,107; 60/176,107; 60/177,731  
; NUMBER OF SEQ ID NOS: 24  
; PRIORITY FILING DATE: 1999-12-23; 2000-01-14; 2000-01-21  
; SOFTWARE: PERL Program  
; SEQ ID NO: 5  
; LENGTH: 798  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: misc. feature  
; NAME/KEY: misc. feature  
; OTHER INFORMATION: Incyte ID No: 2902460CD1  
; US-10-979-095-5

Query Match 66.5%; Score 482; DB 5; Length 1192;  
Best Local Similarity 67.2%; Pred. No. 1.58-44; Matches 92; Conservative 14; Mismatches 31; Indels 0; Gaps 0;  
Matches 92; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

QY 1 AVTKPRYMQMRETMSTSSTLGFRIEGIKKAGTCNTNPKKTOALKVLEDFVGDHV 60 ; APPLICANT: YAO, Monique G.  
Db 869 AVTKPRYMQMRETTISSTATLGFRIEGIKKAGTCNTNPKKTOALKVLEDFVGDHV 928 ; APPLICANT: LAL, Preetai.  
; APPLICANT: KAHN, Farrah A.  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0002 PCT  
; CURRENT APPLICATION NUMBER: US/10/979,095  
; CURRENT FILING DATE: 2004-11-02  
; PRIORITY APPLICATION NUMBER: US/10/168,582  
; PRIORITY FILING DATE: 2002-06-20  
; PRIORITY APPLICATION NUMBER: 60/172,066; 60/176,107; 60/176,107; 60/177,731  
; NUMBER OF SEQ ID NOS: 24  
; PRIORITY FILING DATE: 1999-12-23; 2000-01-14; 2000-01-21  
; SOFTWARE: PERL Program  
; SEQ ID NO: 5  
; LENGTH: 798  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-10-764-330-1

RESULT 7  
US-10-082-830-82  
; Sequence 202, Application US/10082830  
; Publication No. US20030077604A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Yongming  
; APPLICANT: Recipon, Herve  
; APPLICANT: Salceda, Susana  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Turner, Leah  
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Title of Invention: Genes and Proteins  
; FILE REFERENCE: DEX-0249  
; CURRENT APPLICATION NUMBER: US/10/082,830  
; CURRENT FILING DATE: 2001-10-29  
; PRIORITY APPLICATION NUMBER: 60/243,802  
; PRIORITY FILING DATE: 2000-10-27  
; NUMBER OF SEQ ID NOS: 282  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 282  
; LENGTH: 1339  
; ORGANISM: Homo sapiens  
; US-10-082-830-282

Query Match 64.0%; Score 464; DB 4; Length 1339;  
Best Local Similarity 53.1%; Pred. No. 1.8e-42;  
Matches 93; Conservative 14; Mismatches 30; Indels 38; Gaps 1;  
Qy 1 AVTKPRYMQWREMTMSSTSTGPRFEGIK-----28  
Db 1145 AVTKPRYMQWREMTSSTATGPRFEGIKORGSAWGLPTAPGSRPLHPLPQPQVLPV 1204  
Qy 29 -----KADGTCTNTNPKKTQALEQTVKLEDDGDDHVTIQKYVACELERLEISPEF 82  
Db 1205 LSKAAKTRGKGVNDRDFKKTQREQTEAERFKTGKHNLLAYDRDKAIRTTLEVSPP 1264  
Qy 83 KTHEVGSSLIPFVHDITGLAKUMMDPGKTVLPHOTSHRLPWAEGNRGEGYI 137  
Db 1265 KCHEVIGSSLIPFHDKKEQAKVWMDPGKTPPLPREGQTLQHDVWQEGNRGEGYI 1319  
RESULT 8  
US-11-057-143-1725  
; Sequence 1725, Application US/11097143  
; Publication No. US200500208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Verner, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; TITLE OF INVENTION: DROSOPHILA GENES.  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIORITY FILING DATE: 60/157,832  
; PRIORITY APPLICATION NUMBER: 60/160,191  
; PRIORITY FILING DATE: 1999-10-19  
; PRIORITY APPLICATION NUMBER: 60/161,932  
; PRIORITY FILING DATE: 1999-10-28  
; PRIORITY APPLICATION NUMBER: 60/164,769  
; PRIORITY FILING DATE: 1999-11-12  
; PRIORITY APPLICATION NUMBER: 60/173,383  
; PRIORITY FILING DATE: 1999-12-28

Query Match 52.8%; Score 392.5; DB 4; length 316;  
Best Local Similarity 55.1%; Pred. No. 3.9e-34;  
Matches 75; Conservative 19; Mismatches 41; Indels 1; Gaps 1;  
Qy 2 VTKPRYMQWREMTMSSTGPRFEGIKADGTCTNTNPKKTQALEQTVKLEDDGDDHVTIQKYVACELERLEISPEF 61  
Db 149 VTKPRYMQWREMTSSTATGPRFEGIKGKSDGKSSKDPKTTKRNQVTRAPRDFVAGFPHV 208  
Qy 62 LQKVYACELERLEISPEFTHEVWSSSLFVHDITGLAKUMMDPGKTVLPHOTSHRLPWAEGNRGEGYI 121  
Db 209 IPKVNRLRAIRDIVNLSKFTTHEVIGSSLFVHDHSKN-ANIWLLIDPAKTLILPPDIRI 267  
Qy 122 SHRLPWAEGNRGEGYI 137  
Db 268 NHTSEWVWGNHEDGYI 283

RESULT 10  
 US-10-029-386-29832  
 ; Sequence 29832, Application US/10029386  
 ; Publication No. US2003019470A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C  
 ; FILE REFERENCE: AEOMICR-X-2  
 ; CURRENT APPLICATION NUMBER: US/10/029,386  
 ; CURRENT FILING DATE: 2001-12-20  
 ; NUMBER OF SEQ ID NOS: 34288  
 ; SOFTWARE: Adomax Sequence Listing Engine vers. 1.1  
 ; SEQ ID NO 29832  
 ; LENGTH: 71  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: MAP TO CHR19.1  
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.86  
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.69  
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.97  
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1  
 ; OTHER INFORMATION: SWISSPROT HIT: P17105, EVALUE 1.00e-27  
 ; US-10-029-386-29832

Query Match 20.0%; Score 145; DB 4; length 71;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-08;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AVTKPRIMQWETMSSTLPRIGIK 23  
 Db 44 AVTKPRIMQWETMSSTLPRIGIK 71

RESULT 11  
 US-10-408-765A-1520  
 ; Sequence 1520, Application US/10408765A  
 ; Publication No. US2004101874A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Fahy, Eoin D.  
 ; APPLICANT: Zhang, Bing  
 ; APPLICANT: Gibson, Bradford W.  
 ; APPLICANT: Taylor, Steven W.  
 ; APPLICANT: Glenn, Gary M.  
 ; APPLICANT: Warnock, Dale E.  
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
 ; FILE REFERENCE: 660088.455  
 ; CURRENT APPLICATION NUMBER: US/10/408,765A  
 ; CURRENT FILING DATE: 2003-04-04  
 ; NUMBER OF SEQ ID NOS: 3077  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 15220  
 ; LENGTH: 325  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-408-765A-1520

Query Match 11.2%; Score 81.5; DB 4; Length 325;  
 Best Local Similarity 32.7%; Pred. No. 2.7;  
 Matches 32; Conservative 7; Mismatches 26; Indels 33; Gaps 6;  
 Qy 6 RYMQRR-----ETMSST---STIG-----PRIGIKAD-GTCNTNPKIQALEQVTK 49  
 Db 144 RYVVMRMRGILANSYTMESTFGGSTLGNKRDTHPTIDLSLYHVCDT----- 190

RESULT 12  
 US-10-369-493-175  
 ; Sequence 175, Application US/10369493  
 ; Publication No. US20030233675A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Chen, Xianfeng  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
 ; FILE REFERENCE: 38-10(52052)B  
 ; CURRENT APPLICATION NUMBER: US/10/369,493  
 ; CURRENT FILING DATE: 2003-02-28  
 ; PRIORITY APPLICATION NUMBER: US 60/360,039  
 ; PRIORITY FILING DATE: 2002-02-21  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO 175  
 ; LENGTH: 349  
 ; TYPE: PRT  
 ; ORGANISM: Xenorhabdus nematophilus  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1)..(349)  
 ; OTHER INFORMATION: unsure at all Xaa locations  
 ; US-10-369-493-175

Query Match 11.1%; Score 80.5; DB 4; Length 349;  
 Best Local Similarity 24.6%; Pred. No. 3.9;  
 Matches 31; Conservative 24; Mismatches 16; Indels 19; Gaps 6;  
 Qy 14 MSSTLSTLPRIGIKAD--GTCNTN----PKKIQALEQVTKLDPFDVGDVILQK 65  
 Db 191 LSNEPDNDNFKEPDYLSRPDLCDCINISLPNWELFCNDSDIBLISPL----GGKYQFNSY 244

Query Match 6.6%; Score 80.5; DB 4; Length 349;  
 Best Local Similarity 24.6%; Pred. No. 3.9;  
 Matches 31; Conservative 24; Mismatches 16; Indels 19; Gaps 6;  
 Qy 66 VACERLRLAEISPPFKTHEVGSSLFLVHDHGLAKWMDGKTVLVALPDHQLSHRL 125  
 Db 245 AAALBY-AGEEVPKVFKDNIASSDIKIFHFGAPNN-DGEGKAVADKM--HN 299

Query Match 6.6%; Score 80.5; DB 4; Length 349;  
 Best Local Similarity 24.6%; Pred. No. 3.9;  
 Matches 31; Conservative 24; Mismatches 16; Indels 19; Gaps 6;  
 Qy 126 PWAEGN 131  
 Db 300 GQKTN 305

RESULT 13  
 US-11-096-568A-32990  
 ; Sequence 32990, Application US/11096568A  
 ; Publication No. US2006004824A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexandrov, Nickolai et al.  
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
 ; TITLE OF INVENTION: Theory  
 ; FILE REFERENCE: 2750-1592PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096,568A  
 ; CURRENT FILING DATE: 2005-04-01  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO 32990  
 ; LENGTH: 248  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)..(248)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 13601691  
 ; US-11-096-568A-32990

Query Match 11.0%; Score 79.5; DB 6; Length 248;  
 Best Local Similarity 20.5%; Pred. No. 3.2;  
 Matches 31; Conservative 31; Mismatches 44; Indels 45; Gaps 5;

US-11-096-568A-32988

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RESULT 14
US-11-96-568A-32989
; Sequence 32989, Application US/11096568A
; Publication No. US20090482401
Db QY 11 RETNSTSTGFRIEGIKKADGTCTWNFKKTYQALEQTVKLEDFVGDHVILQKYVA--- 67
Db QY 71 KDRQTTVSLGFRVSGPKTFDHOESFWRAEKKL---VLGYNADCARLAKRKFVSSNS 125
Db QY 68 -----CIEERALELPPKTMHEV---GSSLFVHRTG----- 101
Db QY 126 PADSNLTPNCAFASPVYGGENGILAQILEKDWTFOTQLYHENSCSILMIYENESILMQG 185
Db QY 102 -----AKWUMIDFGKTV---ALPDHQTL 121
Db QY 186 GDDARRAPRAGVILKUFAHVIDGNGVIDHNF 216

```

ATTORNEY: ALEXANDROV, NICKOLAI et al.  
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
FILE REFERENCE: 2750-1392PUS2  
CURRENT APPLICATION NUMBER: US/11/096,568A  
CURRENT FILING DATE: 2005-04-01  
NUMBER OF SEQ ID NOS: 34471  
SEQ ID NO 32989  
LENGTH: 300

TYPE: PRT  
ORGANISM: *Arabidopsis thaliana*  
FEATURE: NAME/KEY: misc feature  
LOCATION: (1). (300)  
OTHER INFORMATION: Ceres Seq. ID no. 13601690  
US-11-096-568A-32989

Query Match	11.0%	Score 79.5;	DB 6;	Length 300;
Best Local Similarity	20.5%	Pred. No. 41;		
Matchers	31;	Conservative	31;	Mismatches
QY	11	RETMSTSTGFRIGEKKADCTCNNTFKIQTKALEQVTKLEDFPGDPHIVLQKVA--	67	
	::	:    :    :    :    :    :    :    :    :    :    :    :		
Db	123	KDRQRTTVSISLGRVSGPKIFDHOESSWRAEKKL---VLGYNADGARLALRKPSNS	177	
QY	68	-----CIEBLREALBISPFKTHHV---GSSLIFVHDHITGL---101		
		:    :    :    :    :    :    :    :    :    :    :		
Db	178	PADSNLTPNCAPFASEVYGGCNGNLALAQLKEWTFQTYLHFNSCSILMIYENESILMQG	233	
QY	102	-----AKYWMIDRCKTV---ALPDIQTL 121		
		:    :    :    :    :    :    :    :    :    :    :		
Db	238	GDDAAPAPRAQKLVDFAHVLDDGNGVIDAHNFL 268		

US-11-096-568A-32988

|||||  
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
TITLE OF INVENTION: Therry  
FILE REFERENCE: 2750-1592PUS2  
CURRENT APPLICATION NUMBER: US/11/096,568A  
CURRENT FILING DATE: 2005-04-01  
NUMBER OF SEQ ID NOS: 34471  
SEQ ID NO 32988  
LENGTH: 330  
TYPE: PRT  
ORGANISM: *Arabidopsis thaliana*  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(330)  
OTHER INFORMATION: Ceres Seq. ID no. 13601689

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 21, 2006, 04:27:19 ; Search time 9 Seconds  
 (without alignments)  
 32.516 Million cell updates/sec

Title: US-10-781-581-226

Perfect score: 725  
 Sequence: 1 AVTKPRINQMRQRTMSSTSIL.....HOTLSHRLPWAEGNRGGYL 137

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext: 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 listing first 45 summaries

Database : Published Applications AA New:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaas/US09\_NEW\_PUB\_PEP:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaas/US06\_NEW\_PUB\_PEP:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaas/US07\_NEW\_PUB\_PEP:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaas/US08\_NEW\_PUB\_PEP:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaas/PCT\_NEW\_PUB\_PEP:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaas/US10\_NEW\_PUB\_PEP:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaas/US11\_NEW\_PUB\_PEP:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaas/US60\_NEW\_PUB\_PEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	66.5	9.2	4051	6 US-10-501-834-7
2	65.0	9.0	4059	6 US-10-501-834-6
3	64.8	8.8	194	6 US-10-510-162-4
4	62.4	8.6	2829	6 US-10-525-621-1
5	61.5	8.5	456	6 US-10-705-435A-26
6	61.1	8.4	882	6 US-10-196-749-574
7	60.7	8.3	926	6 US-10-370-959-11
8	59.8	8.1	700	7 US-11-24-999-49
9	58.5	8.1	626	7 US-11-146-700-1
10	58.0	8.1	1866	6 US-10-511-937-2968
11	58.0	8.0	5	7 US-11-264-784-63
12	57.5	7.9	192	6 US-10-505-928-319
13	56.7	7.7	288	6 US-10-705-928-209
14	56.7	7.7	457	6 US-10-705-928-5A-4
15	56.7	7.7	1842	6 US-10-511-937-929
16	55.5	7.6	284	6 US-10-505-928-47
17	55.5	7.6	724	7 US-11-246-999-47
18	54.5	7.5	200	6 US-10-505-928-323
19	54.5	7.5	1722	6 US-10-505-928-780
20	54.5	7.4	529	7 US-11-246-999-29
21	54.5	7.4	748	6 US-10-511-937-3012
22	53.5	7.4	2125	6 US-10-505-928-310
23	53.5	7.3	464	6 US-10-488-015-17
24	53.5	7.3	771	6 US-10-505-928-255
25	52.5	7.2	1722	6 US-10-505-928-65

ALIGNMENTS

RESULT 1  
 US-10-501-834-7

; Sequence 7, Application US/10501834  
 ; Publication No. US2006008828A1

; GENERAL INFORMATION:

; APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,  
 ; APPLICANT: Vicente E.

; TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids

; TITLE OF INVENTION: and Proteins

; FILE REFERENCE: 070509/386US1

; CURRENT APPLICATION NUMBER: US/10/501.834

; CURRENT FILING DATE: 2004-07-19

; PRIOR APPLICATION NUMBER: PCT/US03/02038

; PRIOR FILING DATE: 2003-01-23

; PRIOR FILING DATE: 2002-01-23

; NUMBER OF SEQ ID NOS: 221

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 4051

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-10-501-834-7

Query Match 9.2%; Score 66.5; DB 6; Length 4051;  
 Best Local Similarity 23.2%; Pred. No. 23;  
 Matches 42; Conservative 24; Mismatches 54; Indels 61; Gaps 9;

QY 9 QWRETMWSNSTLGRFRIEGKIKADGTCNTNPK-----KTOALEQVTKC-----49

DB 2449 RWGLTISINNTVNFIDLNKTV-AIRTCSCGSQGGFPVKRQLKFVNSSLVAFPPHAA 2506

QY 50 VLERP-----VQDHLVQLQKVACLEIREALEISPKPK--THEWVQSSLIFVHDITG 100

DB 2507 VQDLDGSLSGKQGKSVL---ASMETLSDTCLTNAFSRQLVSGSYGEAVLFRMIG 2561

QY 101 LAKWMMIDRKGKTVALPD-----HOTLSHRLPWA-----EGNRGGYL 136

DB 2562 LAK--SLODPVKNLWMTDRNRTITINVDTLISNGWMLLQDQETTLQFEGPWTGGS 2619

QY 137 L 137

Sequence 1, AppI

Sequence 2, AppI

Sequence 3, AppI

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Sequence 8, AppI

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Sequence 65

Publication No. US20060088328A1  
 GENERAL INFORMATION:  
 APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,  
 APPLICANT: Vicente E.  
 TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids  
 FILE REFERENCE: 07039/386US1  
 CURRENT APPLICATION NUMBER: US/10/501,834  
 CURRENT FILING DATE: 2004-07-19  
 PRIORITY APPLICATION NUMBER: PCT/US03/02038  
 PRIORITY FILING DATE: 2003-01-23  
 SEQ ID NO: 6  
 LENGTH: 4059  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 PRIORITY FILING DATE: 2002-01-23  
 ORGANISM: Mus musculus  
 FEATURE: NAME/KEY: VARIANT  
 LOCATION: 2511  
 OTHER INFORMATION: Xaa = Pro or Ser  
 FEATURE: NAME/KEY: VARIANT  
 LOCATION: 2981  
 OTHER INFORMATION: Arg or Gln  
 S-10-501-834-6

Query Match 9.0%; Score 65; DB 6; Length 4059;  
 Best Local Similarity 24.1%; Pred. No. 34; Mismatches 51; Indels 48; Gaps 8;  
 Matches 38; Conservative 21; Mismatches 51; Indels 48; Gaps 8;

Y 9 QWRETMSSSTSTGFRIGKIKADGTCNTNFK-----KTOALEQVTK----- 49  
 b 2459 RWELTISNTTFNPF-DGNCVAIRTCGCGPQGGYTVKTRQKFVNSSLVAFXPRAA 2516  
 Y 50 VLEDFV-----VTDGRVILQVYVACELREALEISPPFK---THEVYGSSSLFVHDHTG 100  
 b 2517 VLEDDCGSLSLSKGNSHVL---ASMFLTSIDCLTNASPSQIVPGSVCGEAVLPHRMSIA 2571  
 Y 101 LAKVWMDFGKTVVALPD-----HOTLSHRLPN 127  
 b 2572 LAN-----SDVPKNLTITDISNKITVNTVYEDTISNYGWN 2607

ESULT 3  
 S-10-510-162-4  
 Sequence 4, Application US/10510162  
 Publication No. US20060099580A1  
 GENERAL INFORMATION:  
 APPLICANT: Corena T. McMANUS  
 APPLICANT: David A. JONES  
 TITLE OF INVENTION: METHYL-GPG BINDING DOMAIN PROTEIN 2 HOMOLOGS  
 FILE REFERENCE: 38509-0016US1  
 CURRENT APPLICATION NUMBER: US/10/510,162  
 CURRENT FILING DATE: 2004-10-05  
 PRIORITY APPLICATION NUMBER: PCT/US03/10631  
 PRIORITY FILING DATE: 2003-04-07  
 PRIORITY APPLICATION NUMBER: 60/369,851  
 PRIORITY FILING DATE: 2002-04-05  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 4  
 LENGTH: 194  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 S-10-510-162-4

RESULT 4  
 S-10-525-621-1  
 Sequence 1, Application US/10525621  
 Publication No. US20060100418A1  
 GENERAL INFORMATION:  
 APPLICANT: Kiyosue, Yuko  
 APPLICANT: Saasaki, Hiroyuki  
 APPLICANT: Tsukita, Shochiro  
 APPLICANT: Eisai Co., Ltd.  
 TITLE OF INVENTION: CULTURED XENOPUS LAEVIS CELL LINES  
 TITLE OF INVENTION: EXPRESSING MUTANT ADENOMATOUS POLYPOSIS COLI GENE  
 FILE REFERENCE: 082368-024400US  
 CURRENT APPLICATION NUMBER: US/10/525,621  
 CURRENT FILING DATE: 2005-02-22  
 PRIORITY APPLICATION NUMBER: PCT/JP03/10434  
 PRIORITY FILING DATE: 2003-08-19  
 PRIORITY APPLICATION NUMBER: JP 2002-241487  
 PRIORITY FILING DATE: 2002-08-22  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 1  
 LENGTH: 2829  
 TYPE: PRT  
 ORGANISM: Xenopus laevis  
 US-10-525-621-1

Query Match 8.6%; Score 62; DB 6; Length 2829;  
 Best Local Similarity 24.2%; Pred. No. 48; Mismatches 43; Indels 16; Gaps 8;  
 Matches 24; Conservative 16; Mismatches 43; Indels 16; Gaps 8;

QY 5 PRYMMORETMSSTSTGFRIGKIKAD-----GTCNTNFKKTOALEQVTK 49  
 Db 2553 PRVSTWRIGTSSSILSASSESEKASEDBQQVCSFPGRSECSSAKGTVRKIKSE 2651  
 QY 50 VLEDFVGDVILQVYVACELREALEISPPFK---FFKTHEV 87  
 Db 2613 ILETPSNGSSSTTAESNCSLSKTLVYQMAPAVSKTEDV 2651

RESULT 5  
 US-10-706-435A-26  
 Sequence 26, Application US/10706435A  
 Publication No. US20060088547A1  
 GENERAL INFORMATION:  
 APPLICANT: Walter Reed Army Institute of Research  
 APPLICANT: Lanier, David E.  
 APPLICANT: Hillier, Collette J.  
 APPLICANT: Lyon, Jeffrey A.  
 APPLICANT: Angov, Evelina  
 APPLICANT: Kumar, Sanjai  
 APPLICANT: Rogers, William  
 APPLICANT: Barbosa, Arnoldo  
 TITLE OF INVENTION: Expression, Purification, and Uses of a Plasmodium  
 TITLE OF INVENTION: Placparum Liver Stage Antigen 1 Polypeptide  
 FILE REFERENCE: 003/285/SAP  
 CURRENT APPLICATION NUMBER: US/10/706,435A  
 CURRENT FILING DATE: 2003-11-12  
 PRIORITY APPLICATION NUMBER: 60/435,719  
 PRIORITY FILING DATE: 2002-11-12  
 NUMBER OF SEQ ID NOS: 28  
 SOFTWARE: Microsoft Word XP  
 SEQ ID NO: 26  
 LENGTH: 456  
 TYPE: PRT

Query Match 8.8%; Score 64; DB 6; Length 194;  
 Best Local Similarity 25.3%; Pred. No. 0.71; Mismatches 36; Indels 18; Gaps 6;  
 Matches 25; Conservative 20; Mismatches 36; Indels 18; Gaps 6;

Query Match ; ORGANISM: Artificial sequence  
; FEATURE: ; OTHER INFORMATION: LSA-NRC(H) protein  
; US-10-706-435A-26

Query Match Best Local Similarity 8.5%; Score 61.5; DB 6; Length 456; Matches 28; Conservative 15; Mismatches 25; Indels 27; Gaps 5; RESULT 6

US-10-196-749-574 ; Sequence 574, Application US/10196749 ; Publication No. US200600948641 ; GENERAL INFORMATION: ; APPLICANT: Baker, Kevin P.

Qy 23 RIEGIRKADGTCNTNP-----KIQQAQLEVKVLEDFV-----DGPVHILQ 63 ; Publication No. US20060088907A1 ; GENERAL INFORMATION: ; APPLICANT: Chen, Jian ; APPLICANT: Desnoyers, Luc ; APPLICANT: Goddard, Audrey ; APPLICANT: Godowski, Paul J. ; APPLICANT: Gurney, Austin L. ; APPLICANT: Pan, James ; APPLICANT: Smith, Victoria ; APPLICANT: Watnabe, Colin K. ; APPLICANT: Zhang, Zemin

Db 369 KIKKGKRYEKTKDNKRNPKNDLSYDNEHIIKKYKDNKVKNKEKFKTSFLHIFDGDNEILQ 428 ; APPLICANT: Millennium Pharmaceuticals, Inc ; APPLICANT: Meyers, Rachel E. ; APPLICANT: Williamson, Mark W. ; APPLICANT: Kapeller-Libermann, Rosana ; APPLICANT: MacBeth, Kyle J. ; APPLICANT: Hunter, John J. ; APPLICANT: Rudolph-Owen, Laura A. ; APPLICANT: Bandaru, Rakeshkar

Qy 64 KVVACLERLRAALEISPPPKTHEVVGSSLLVHDH 98 ; Publication No. US10370959 ; GENERAL INFORMATION: ; APPLICANT: Tsai, Fong-Ying

Db 429 ---IVDELSE--DITKYM--KLGGSFPHHH 455 ; TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677, 55562, 39228, 26320, 46619, 33166, 18336, 46867, 21617, 55562, 39228, 32258, 46863 AND TITLE OF INVENTION: 32252 MOLECULES AND USES THEREFOR ; FILE REFERENCE: MP103-0170NTM ; CURRENT APPLICATION NUMBER: US/10/370, 959 ; CURRENT FILING DATE: 2003-02-20 ; PRIOR APPLICATION NUMBER: US 09/910,150 ; PRIOR FILING DATE: 2001-07-18 ; PRIOR APPLICATION NUMBER: US 60/219, 028 ; PRIOR FILING DATE: 2000-07-18 ; PRIOR APPLICATION NUMBER: US 10/251, 507 ; PRIOR FILING DATE: 2002-09-20 ; PRIOR APPLICATION NUMBER: US 09/715, 479 ; PRIOR FILING DATE: 2000-11-17 ; PRIOR APPLICATION NUMBER: US 60/218, 053 ; PRIOR FILING DATE: 2000-07-13 ; PRIOR APPLICATION NUMBER: US 09/644, 929 ; PRIOR FILING DATE: 2000-08-23 ; PRIOR APPLICATION NUMBER: US 60/212, 439 ; PRIOR FILING DATE: 2000-06-15 ; PRIOR APPLICATION NUMBER: US 09/892, 870 ; PRIOR FILING DATE: 2001-06-25 ; PRIOR APPLICATION NUMBER: US 60/214, 174 ; PRIOR FILING DATE: 2000-06-26 ; PRIOR APPLICATION NUMBER: US 09/775, 117 ; PRIOR FILING DATE: 2001-02-01 ; Remaining Prior Application data removed - See File Wrapper or PALM. ; NUMBER OF SEQ ID NOS: 156 ; SOFTWARE: FASTSEQ for Windows Version 4.0 ; SEQ ID NO 11 ; LENGTH: 926 ; TYPE: PRT ; ORGANISM: Homo Sapiens

US-10-370-959-11 ; Query Match Best Local Similarity 8.3%; Score 60; DB 6; Length 926; Matches 26; Conservative 16; Mismatches 42; Indels 16; Gaps 3; NUMBER OF SEQ ID NOS: 612 ; SEQ ID NO 574 ; LENGTH: 882 ; TYPE: PRT ; ORGANISM: Homo Sapien

Query Match Best Local Similarity 8.4%; Score 61; DB 6; Length 882; Matches 21; Conservative 14; Mismatches 41; Indels 6; Gaps 3; RESULT 8

Qy 28 KKAQTCWTFNKKIQALEQWTKVLEDFVQDHV--ILQKY--VACLERLRAALEISPPF 82 ; Sequence 82, Application US/11246999



```

; APPLICANT: Raghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3135 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 63
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Candida albicans (GenBank Accession No. FAL04510)
; US-11-264-784-63

Query Match 8.0%; Score 58; DB 7; Length 353;
Best Local Similarity 23.9%; Pred. No. 8.6; Mismatches 21; Conservative 21; Indels 30; Gaps 7;
Matches 21; Mismatches 21; Indels 30; Gaps 7;

Qy 50 VLEDFYDGHYILOKY--VAGLEELRALESPFEEK-----THEVGSSLFLFVHDKT 99
Db 245 VFNFSF---HSWYFPLSLK---IRVNPFFERILTMQIQTIVGEGSIAIHLHF- 295
Qy 100 GLAKVMMIDFCVKTVALPDHQTLISHRIFW 127
Db 296 ---VWIVDTSHVIS-PDN-----LKW 312

RESULT 12
US-10-505-928-519
; Sequence 519 Application US/10505928
; Publication No. US20050088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIORITY APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO: 519
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-519

Query Match 7.9%; Score 57.5; DB 6; Length 192;
Best Local Similarity 25.2%; Pred. No. 4.3; Matches 26; Conservative 23; Mismatches 45; Indels 9; Gaps 4;
; Gaps 4;

Qy 8 MQRWETMSSSTLSPFRIEGKIKADGTC--NTNEFKTQALEQVVKLRF--VDG-DHV 60
Db 33 LKFNFBFVNTPVPTGFTKIKLNSGTAKGISCHFWDVGQOBKLRLWKSYSRCTDGIYV 92
Qy 61 ILQKVACLELREALEISFFKTHEVGSSLFLFHDTGLAK 103
Db 93 VSDVVDVDRLEAK--TELHKVTKFAENQGTPLVANKQDLPK 133

RESULT 13
US-10-505-928-209
; Sequence 209 Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27

Query Match 7.7%; Score 56; DB 6; Length 457;
Best Local Similarity 27.4%; Pred. No. 21; Matches 26; Conservative 16; Mismatches 27; Indels 26; Gaps 4;
; Gaps 4;

Qy 23 RIEGKIKADGTCTNTP-----KKTQALEQVVKLRF--DGDHVILQ 63
Db 369 KIKGGKKTEKTKONFKNDKSLYDEHKKYNQKQNEKEFPIKSLFHIFGDGNEILQ 428
Qy 64 KVACLELREALEISFFKTHEVGSSLFLFHDTGLAK 98
Db 429 ----IVDRLSEDITKPFM-KUGGSSPHHH 456

RESULT 15
US-10-511-937-2929
; Sequence 2929 Application US/10511937

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Publication No. US20060088836A1  
 GENERAL INFORMATION:  
 APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
 APPLICANT: Wohlgemuth, Jay  
 APPLICANT: FRY, Kirk  
 APPLICANT: Woodward, Robert  
 APPLICANT: Ly, Ngoc  
 APPLICANT: Prentice, James  
 APPLICANT: Morris, Macdonald  
 APPLICANT: Rosenberg, Steven  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
 TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
 FILE REFERENCE: 506612000104  
 CURRENT APPLICATION NUMBER: US/10/511, 937  
 CURRENT FILING DATE: 2004-10-19  
 PRIOR APPLICATION NUMBER: PCT/US2003/012946  
 PRIOR FILING DATE: 2003-04-24  
 PRIOR APPLICATION NUMBER: US 10/131, 831  
 PRIOR FILING DATE: 2002-04-24  
 PRIOR APPLICATION NUMBER: US 10/325, 899  
 PRIOR FILING DATE: 2002-12-20  
 NUMBER OF SEQ ID NOS: 3117  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 2929  
 LENGTH: 1842  
 TYPE: PRT  
 ORGANISM: *Homo sapiens*  
 US-10-511-937-2929

Query Match 7.7%; Score 56; DB 6; Length 1842;  
 Best Local Similarity 27.7%; Pred. No. 1.4e+02; Gaps 8;  
 Matches 28; Conservative 16; Mismatches 29; Indels 28; Gaps 8;  
 Matches 28;

Qy	38	FKKTOA---LEQTTKVLDFPV---DGHVTIQL-KYVACLEERALELISP-----FRT	84
Db	860	KKKQBCRDILIPVITKELKELQKUDMQRQVLLERY-CVELLSILSLEVSIQDAFTY	917
Qy	85	HEV--VGSSILFVHDHTGLAKVMMIDFGKVALDPQTISH	123
Db	918	HHQIBIMVQIIRNT-----VITMGR-----DHLISH	947

Search completed: May 21, 2006, 04:30:20  
 Job time : 9 secs